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OM nucleic - nucleic search, using sw model

Run on: September 23, 2005, 13:10:50 ; Search time 5974 Seconds  
(without alignments)  
11168.870 Million cell updates/sec

Title: US-10-811-170-1  
Perfect score: 1377  
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Scoring table: IDENTITY NUC

Gapop 10\_0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_htg.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

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11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1377	100.0	1377	6	AX056749	AX056749 Sequence
2	1328.4	96.5	1453	6	AX056745	AX056745 Sequence
3	1049.2	76.2	1444	6	AX056747	AX056747 Sequence
4	1039	75.5	1359	6	AX056739	AX056739 Sequence
5	1032.4	75.0	1389	6	AX056741	AX056741 Sequence
6	987.4	71.7	1674	6	AX056737	AX056737 Sequence
7	982.4	71.3	1704	6	AX056743	AX056743 Sequence
8	980.8	71.2	1704	6	AX056735	AX056735 Sequence
9	687.2	49.9	1383	6	AX338526	AX338526 Sequence
10	686	49.8	2043	6	AR112718	AR112718 Sequence
11	684	49.7	705	6	AR380678	AR380678 Sequence
12	684	49.7	762	6	AX556168	AX556168 Sequence
13	684	49.7	1019	6	AR137115	AR137115 Sequence
14	684	49.7	1019	6	BD271954	BD271954 Cell surf
15	684	49.7	1019	6	AR275187	AR275187 Sequence
16	684	49.7	1159	9	HSAL17957	Y17957 Homo sapien
17	684	49.7	1182	6	AR173440	AR173440 Sequence
18	684	49.7	1182	6	CQ857740	CQ857740 Sequence
19	684	49.7	1356	6	AX357970	AX357970 Sequence

ALIGNMENTS

RESULT 1	AX056749	1377 bp	DNA	linear	PAT 17-JAN-2001
LOCUS	Sequence 15 from Patent WO0075319.				
DEFINITION	AX056749				
ACCESSION	AX056749.1				
VERSION	GI:12309728				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens				
REFERENCE	1				
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
TITLE	Papadopoulos,N.J., Davis,S. and Yancopoulos,G.D.				
JOURNAL	Modified chimeric polypeptides with improved pharmacokinetic properties				
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Query Match 100.0%; Score 1377; DB 6; Length 1377;  
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RESULT 2  
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LOCUS  
DEFINITION  
AX056745  
ACCESSION  
VERSION  
AX056745.1 GI:12309724  
SOURCE  
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ORGANISM  
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
  
REFERENCE  
1  
Papadopoulos,N.J., Davis,S. and Yancopoulos,G.D.  
Modified chimeric polypeptides with improved pharmacokinetic  
properties  
Patent: WO 0075319-A 11 14-DEC-2000;  
REGENERON PHARMACEUTICALS, INC. (US)  
  
JOURNAL  
Location/Qualifiers  
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DEFINITION Sequence 5 from Patent WO0075319.  
ACCESSION AX056739  
VERSION AX056739.1 GI:12309718  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
AUTHORS Papadopoulos,N.J., Davis,S. and Yancopoulos,G.D.  
TITLE Modified chimeric polypeptides with improved pharmacokinetic properties  
JOURNAL Patent: WO 0075319-A 5 14-DEC-2000;  
REGENERON PHARMACEUTICALS, INC. (US)

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Query Match 75.5%; Score 1039; DB 6; Length 1359;  
Best Local Similarity 86.3%; Pred. No. 3.4e-231;  
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DEFINITION Sequence 1 from Patent WO0075319.  
ACCESSION AX056735  
VERSION AX056735.1 GI:12309714  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
Papadopoulos,N.J., Davis,S. and Yancopoulos,G.D.  
AUTHORS Modified chimERIC polypeptides with improved pharmacokinetic  
TITLE properties  
JOURNAL Patent: WO 0075319-A 1 14-DEC-2000;  
REGENERON PHARMACEUTICALS, INC. (US)  
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PIEKTLSKAKGQRPQVYTLPPSRDELTKNOVSLTCLVKGYFPPSDIAVEWESNGOPE  
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Query Match 71.2%; Score 980.8; DB 6; Length 1704;  
Best Local Similarity 85.3%; Pred. No. 1.2e-217;  
Matches 1131; Conservative 0; Mismatches 162; Indels 33; Gaps 2;

ORIGIN

QY 79 AGTGATACCGGTAGACCTTTTCGTAGAGATGTACAGTGAATAATCCCGGAAATTATACATG 138  
Db 385 AGTGATACAGGTAGACCTTTTCGTAGAGATGTACAGTGAATAATCCCGGAAATTATACATG 444  
QY 139 ACTGAAGGAAGGAGCTCGTCATTTCCCTCCCGGTTACGTCACTTAACATCACTGTACT 198  
Db 445 ACTGAAGGAAGGAGCTCGTCATTTCCCTCCCGGTTACGTCACTTAACATCACTGTACT 504  
QY 199 TTAATAAAAGTTTCCACTTCGACACTTTTGATCCCTGATGGAAAAACGCATAATCTGGGACAGT 258  
Db 505 TTAATAAAAGTTTCCACTTCGACACTTTTGATCCCTGATGGAAAAACGCATAATCTGGGACAGT 564  
QY 259 AGAAAGGGCTTCATCATATCAATCAACGTAACAAGAAATAGGGCTTCTGACCTGTGAA 318  
Db 565 AGAAAGGGCTTCATCATATCAATCAACGTAACAAGAAATAGGGCTTCTGACCTGTGAA 624  
QY 319 GCAACAGTCAATGGGCACTTTGTATAAGCAAACTATCTCACATCGACAAACCAATACA 378  
Db 625 GCAACAGTCAATGGGCACTTTGTATAAGCAAACTATCTCACATCGACAAACCAATACA 684  
QY 379 ATCATAGATGTGGTTCGTAGTCCGTCTCATGGAATTTGAATCTCTGTCGAGAAAAAGCTT 438  
Db 685 ATCATAGATGTCCAATAAGACACACGCCAGTCAAAATTACTTAGAGGCCATCTCTT 744  
QY 439 GTCTTTAAATTTGACAGCAAGAACTGAACCTAAATTTGGGGAATGACCTTCAACTGGGAATAC 498  
Db 745 GTCTCTCAATTTGACTGTACCACTCCCTTTGAACACGAGAGTTCAAAATGACCTGGAGTTAC 804  
QY 499 CTTCTTCCGAGCATCAGCATAAAGAACTTTGAAACCGAGACCTTAAAAACCCAGTCTGGG 558  
Db 805 CCT-----GATGAAAAAATAAGAGAGCTTCCTGTAAGCGCAGCAATTGACCAAGCAAT 858  
QY 559 AGTGAGATGAAGAAATTTTGTAGACACCTTAACTATAGATGGTGTAAACCCGAGTAGCCAA 618  
Db 859 TCCCATGCCACATATTTCTACAGTGTCTTACTATTGACAAAATGCAGAACAAAGACAA 918  
QY 619 GGATTTGACACCTGTGACAGCATCCAGTGGGTGTGATGACCAAGAAACAGCACATTTTTC 678  
Db 919 GGACTTTTATCTGTGTGTAAGGAGTGGACCATCATTCAAATCTGTTAAACACCTCAGTG 978  
QY 679 AGGGTCCATGAAA-----GGACAAAACCTCACATGC 711  
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QY 712 CCACCGTGCCAGCACCTGAACTCTCTGGGGGACCGTCACTCTCTCTTCCCCCAAAA 771  
Db 1039 CCACCGTGCCAGCACCTGAACTCTCTGGGGGACCGTCACTCTCTCTTCCCCCAAAA 1098  
QY 772 CCCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTCACTAGGTGATGAGTGGACGTTG 831  
Db 1099 CCCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTCACTAGGTGATGAGTGGACGTTG 1158  
QY 832 AGCCAGGAAGACCTTGAGGTCAAGTTCACTGGTAGTGGACGGCGTGGAGGTGCATAT 891  
Db 1159 AGCCAGGAAGACCTTGAGGTCAAGTTCACTGGTAGTGGACGGCGTGGAGGTGCATAT 1218  
QY 892 GCAAGACAAAACCCCGGAGGAGCAGTACAAACAGCACCTACCGTGTGTGTGACGCGTCTC 951  
Db 1219 GCAAGACAAAACCCCGGAGGAGCAGTACAAACAGCACCTACCGTGTGTGTGACGCGTCTC 1278  
QY 952 ACCGTCTCTGCACAGGACTGGCTGAATGCAAGGAGTACAAGTGAAGTGTCTCCAAACAA 1011  
Db 1279 ACCGTCTCTGCACAGGACTGGCTGAATGCAAGGAGTACAAGTGAAGTGTCTCCAAACAA 1338









PC	C12N15/09, A61K9/48, A61K38/00, A61K39/395, A61K48/00, A61P1/04, PC A61P1/16,
PC	A61P3/10, A61P7/06, A61P9/02, A61P11/02, A61P11/06, A61P17/00, PC A61P17/05,
PC	A61P19/02, A61P21/02, A61P21/04, A61P25/00, A61P35/00, A61P37/02, PC A61P37/06,
PC	C07K14/705, C07K16/46, C07K19/00, C12N5/10, C12N15/00, C12N5/00, PC A61K37/02
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CDS	Location/Qualifiers
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	/mol_type="genomic DNA"
	/db_xref="taxon:9606"
FEATURES	
source	

ORIGIN	Query Match	49.7%	Score 684;	DB 6;	Length 1019;	
	Best Local Similarity	100.0%;	Pred. No. 1.7e-148;			
	Matches 684;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy	694	GACAAAAC	TACACAT	CCCCAC	CGTGC	CCCGAGCACCTGAACTCTCTGGGGGACCGTCAAGTC 753
Db	328	GACAAAAC	TACACAT	CCCCAC	CGTGC	CCCGAGCACCTGAACTCTCTCTGGGGGACCGTCAAGTC 387
Qy	754	TTCCCTCT	TTCGCC	CCAAAAC	CCAGGAC	CACCGTCAATGATCTTCCCGGACCCCTGAGGTCAACA 813
Db	388	TTCCCTCT	TTCGCC	CCAAAAC	CCAGGAC	CACCGTCAATGATCTTCCCGGACCCCTGAGGTCAACA 447
Qy	814	TGCGTG	TGTTGG	ACGTGAG	CCACGAG	ACCCCTGAGGTCAGGTCAACTGGTACGTCGAC 873
Db	448	TGCGTG	TGTTGG	ACGTGAG	CCACGAG	ACCCCTGAGGTCAACTGGTACGTCGAC 507
Qy	874	GGCGTG	GAGGTGC	ATAATG	CCACG	ACAAAGCCGGGAGGAGCAGTACAAACAGCACGCTAC 933
Db	508	GGCGTG	GAGGTGC	ATAATG	CCACG	ACAAAGCCGGGAGGAGCAGTACAAACAGCACGCTAC 567
Qy	934	CGTGTG	GTCA	GGCTCT	CGAC	CCAGGACTGGGTGAAATGGCAAGGAGTACAAG 993
Db	568	CGTGTG	GTCA	GGCTCT	CGAC	CCAGGACTGGGTGAAATGGCAAGGAGTACAAG 627
Qy	994	TGCAAG	GTCTCC	AAACAA	AGCCCT	CCCCAGCCCCCATCGAGAAAAACATCTTCCAAAGCCAAA 1053
Db	628	TGCAAG	GTCTCC	AAACAA	AGCCCT	CCCCAGCCCCCATCGAGAAAAACATCTTCCAAAGCCAAA 687
Qy	1054	GGG	CAGCCCCG	GAGAAC	CACAG	GTGTACACCTTGCCCCCATCCCGGGATGAGTCAACCAAG 1113
Db	688	GGG	CAGCCCCG	GAGAAC	CACAG	GTGTACACCTTGCCCCCATCCCGGGATGAGTCAACCAAG 747
Qy	1114	AAC	CAGGTG	ACGCTG	CTGGT	CAAAAGGCTTCTATCCACGGACATCGCCGTCGAG 1173
Db	748	AAC	CAGGTG	ACGCTG	CTGGT	CAAAAGGCTTCTATCCACGGACATCGCCGTCGAG 807
Qy	1174	TGG	GAGAGCA	ATGGG	CAGCCG	GAGAAACAACTTACAAGACCAACGCTCCCGTGTGGAATCC 1233
Db	808	TGG	GAGAGCA	ATGGG	CAGCCG	GAGAAACAACTTACAAGACCAACGCTCCCGTGTGGAATCC 867
Qy	1234	GAC	GGCTCCTT	CTTCTCT	ACAG	CAAGCTCACCGTTGGACAAAGACAGTGGCAGCAGGGG 1293
Db	868	GAC	GGCTCCTT	CTTCTCT	ACAG	CAAGCTCACCGTTGGACAAAGACAGTGGCAGCAGGGG 927
Qy	1294	AAC	GTCTTCT	CAATG	CTCG	TGATGATGAGGCTCTGCAACCAACTTACACGCAAGAGC 1353
Db	928	AAC	GTCTTCT	CAATG	CTCG	TGATGATGAGGCTCTGCAACCAACTTACACGCAAGAGC 987
Qy	1354	CTCT	CCCTGTCT	CCGGTAA	ATGA 1377	
Db	988	CTCT	CCCTGTCT	CCGGTAA	ATGA 1011	

RESULT 15  
AR275187

Search completed: September 23, 2005, 15:40:24  
Job time : 5983 secs

LOCUS	AR275187	1019 bp	DNA	linear	PAT 10-APR-2003
DEFINITION	Sequence	1 from patent US 6506891.			
ACCESSION	AR275187				
VERSION	AR275187.1	GI:29708174			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
	Unclassified.				
REFERENCE	1 (bases 1 to 1019)				
AUTHORS	Tao, W., Wong, S., Hickey, W. F., Hammang, J. P. and Baetge, E. E.				
TITLE	Cell surface molecule-induced macrophage activation				
JOURNAL	Patent: US 6506891-A 1 14-JAN-2003;				
FEATURES	Location/Qualifiers				
source	1..1019				
	/organism="unknown"				
	/mol_type="genomic DNA"				

ORIGIN	Query Match	49.7%;	Score 684;	DB 6;	Length 1019;
	Best Local Similarity	100.0%;	Pred. No. 1.7e-148;		
	Matches 684;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	694	GACAAACTCACACATGCCCCACCGTCCCAAGCAGCTGAATCTCTGGGGGACCGTCAATC	753		
Db	328	GACAAAACTCACACATGCCCAACCGTCCCAAGCAGCTGAATCTCTGGGGGACCGTCAATC	387		
Qy	754	TTCTCTTTCCTCCCAAAACCCAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTCAACA	813		
Db	388	TTCTCTTTCCTCCCAAAACCCAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTCAACA	447		
Qy	814	TGGTGTGTGTGGAGCTGAGCCAGCAAGACCCCTGAGGTCAAGTTCAACTGGTAGTGGAC	873		
Db	448	TGGTGTGTGTGGAGCTGAGCCAGCAAGACCCCTGAGGTCAAGTTCAACTGGTAGTGGAC	507		
Qy	874	GGCTGTGAGGTGCAATATGTCAAGCAAAAGCCGCGGAGGAGCAGTACAAACAGCAGCTAC	933		
Db	508	GGCTGTGAGGTGCAATATGTCAAGCAAAAGCCGCGGAGGAGCAGTACAAACAGCAGCTAC	567		
Qy	934	CGTGTGTGTGAGCGTCTTACCGTCTGTGCACAGGACTGGCTGAATGCCAAGGAGTACAAG	993		
Db	568	CGTGTGTGTGAGCGTCTTACCGTCTGTGCACAGGACTGGCTGAATGCCAAGGAGTACAAG	627		
Qy	994	TGCAGGTCTCCAAACAAAGCCCTCCAGCCCCCATCGAGAAAAACCATCTCCAAAGCCAAA	1053		
Db	628	TGCAAGGTCTCCAAACAAAGCCCTCCAGCCCCCATCGAGAAAAACCATCTCCAAAGCCAAA	687		
Qy	1054	GGGAGCCCCGAGAACACACAGGTGTACACCTTCGCCCCATCCCGGGATGAGCTGACCAAG	1113		
Db	688	GGGAGCCCCGAGAACACACAGGTGTACACCTTCGCCCCATCCCGGGATGAGCTGACCAAG	747		
Qy	1114	AACAGGTTCAGCCTGACCTGCCTGGTCAAAAGGCTTCTATCCACGACACATCGCCGTGGAG	1173		
Db	748	AACAGGTTCAGCCTGACCTGCCTGGTCAAAAGGCTTCTATCCACGACACATCGCCGTGGAG	807		
Qy	1174	TGGGAGAGCAATGGGACCGCGAGAACAACTACAAGACCAACGCTCCCGTCTGAGTCC	1233		
Db	808	TGGGAGAGCAATGGGACCGCGAGAACAACTACAAGACCAACGCTCCCGTCTGAGTCC	867		
Qy	1234	GACGGTCTCTTCTTCTTCTACAGCAAGCTCAACCGTGGACAAAGACAGCTGGCAGCAGGG	1293		
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Qy	1294	AACGTCTTCTCATGCTCCGTGATGCATGAGGCTTCGACAAACCACTACAGCAGCAAGAGC	1353		
Db	928	AACGTCTTCTCATGCTCCGTGATGCATGAGGCTTCGACAAACCACTACAGCAGCAAGAGC	987		
Qy	1354	CTCTCCCTGTCTCCGGGTAAATGA	1377		
Db	988	CTCTCCCTGTCTCCGGGTAAATGA	1011		

Search completed: September 23, 2005, 15:40:24  
Job time : 5983 secs

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XX This semence encodes a fusion protein of the invention between the Flt1

CC receptor and the Fc region of IgG. The specification relates to modified  
CC chimeric polypeptides with improved pharmacokinetics. The modified  
CC chimeric polypeptides are preferably Flt1 receptor polypeptides that have  
CC been modified to improve their pharmacokinetic profile. The polypeptides  
CC can be used to decrease or inhibit plasma leakage and/or vascular  
CC permeability in a mammal  
XX  
SQ

Sequence 1377 BP; 386 A; 374 C; 339 G; 278 T; 0 U; 0 Other;

Query Match 100.0%; Score 1377; DB 5; Length 1377;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 121 CCCGAAATTATACATGATGCTGAAGGAAGGAGCTCGTCAATCCCTGCCGGGTTACGTCA 180  
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DB 181 CCTAACATCACTGTTACTTTAAAAAGTTTCCACTTGGACACTTTGATCCCTGATGGAATA 240  
QY 241 CGCATATCTGGGACAGTGAAGGGCTTCATCATATCAATGCAAGTACAAAGAAATA 300  
DB 241 CGCATATCTGGGACAGTGAAGGGCTTCATCATATCAATGCAAGTACAAAGAAATA 300  
QY 301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATGAAGCAAACTATCTCACA 360  
DB 301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATGAAGCAAACTATCTCACA 360  
QY 361 CATCGCAAAACCAATCAATAGATAGTGGTTCTGAGTCCGCTCATGGAATTTGAACATA 420  
DB 361 CATCGCAAAACCAATCAATAGATAGTGGTTCTGAGTCCGCTCATGGAATTTGAACATA 420  
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QY 481 GACTTCAACTGGGAATACCTTCTTCGAAGCATCAGCATGAAGAACTTGTAAACCGAGAC 540  
DB 481 GACTTCAACTGGGAATACCTTCTTCGAAGCATCAGCATGAAGAACTTGTAAACCGAGAC 540  
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DB 601 GTAAACCCGGAGTGACCAAGGATTTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660  
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QY 901 AAGCCGCGGAGGAGCAGTACACACAGCTACCGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGT 960  
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QY 1321 GAGGCTCTGCACAAACCATCTACACGCAAGAGAGCTCTCCCTGTCTCCGGGTAAATGA 1377  
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RESULT 2  
ABQ74610

ID ABQ74610 standard; cDNA; 1377 BP.

XX AC ABQ74610;

XX DT 23-OCT-2002 (first entry)

XX Modified Flt1 receptor VEGFR1R2-FcDELTA1(a) nucleotide sequence.

Human; Flt1; vascular endothelial growth factor; VEGF; VEGF antagonist;  
psoriasis; wound healing; Flt1 receptor; antipsoriatic; antiinflammatory;  
vulnerary; antiasthmatic; antirheumatic; antiarthritic; nephrotropic;  
ophthalmological; vascular permeability; oedema; inflammation; asthma;  
brain oedema; inflammatory disorder; rheumatoid arthritis; burn;  
kidney disease; eye disorder; age-related macular degeneration;  
diabetic retinopathy; gene; ss.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

XX CDS 1..1377

XX FT /tag= a

XX FT /product= "VEGFR1R2-FcDELTA1(a)"

XX PN WO200260489-A1.

XX PD 08-AUG-2002.

XX PF 28-JAN-2002; 2002WO-US002466.

XX PR 31-JAN-2001; 2001US-00773877.

XX PA (REGE-) REGENERON PHARM INC.

XX PI Xia Y, Rudge JS, Yancopoulos GD;

XX WPI; 2002-608488/65.

DR P-PSDB; ABP52449.

XX Treating psoriasis and enhancing wound healing in humans comprises the  
PT administration of a vascular endothelial cell growth factor (VEGF)  
XX antagonist.  
XX  
XX Example 20; Fig 24A-C; 179pp; English.  
XX  
XX The present invention describes a method for treating psoriasis and  
XX enhancing wound healing in a mammal or a human. The method comprises  
XX administering a vascular endothelial cell growth factor (VEGF) antagonist  
XX to the mammal or human. A VEGF antagonist has antipsoriatic, antiarthritic,  
XX antiinflammatory, vulnery, antiasthmatic, antirheumatic, antiarthritic,  
XX nephrotropic and ophthalmological activities. The method can be used in  
XX treating psoriasis and enhancing wound healing in humans by administering  
XX VEGF antagonist. The method is also useful in treating clinical  
XX conditions characterised by vascular permeability, oedema or  
XX inflammation, such as brain oedema associated with injury, oedema  
XX associated with inflammatory disorders (e.g. rheumatoid arthritis),  
XX asthma, burns, kidney diseases, or eye disorders such as age-related  
XX macular degeneration and diabetic retinopathy. The method may also be  
XX used in making the polypeptide to decrease or inhibit plasma leakage and  
XX or vascular permeability. The present sequence encodes VEGFR1R2-  
XX FcDELUTACI(a) which is used in an example from the present invention  
XX  
XX Sequence 1377 BP; 386 A; 374 C; 339 G; 278 T; 0 U; 0 Other;  
XX  
XX Query Match 100.0%; Score 1377; DB 6; Length 1377;  
XX Best Local Similarity 100.0%; Pred. No. 0;  
XX Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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XX 601 GTHAACCCGGAGTGACCAAGATTGTACACTGTGCGAGATCCAGTGGGCTGATGACCAAG 660

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QY 781 ACCCTCATGATCTCCCGGACCCCTGAGGTACACATGGTGTGGTGTGAGCGTGGAGCCAGAA 840  
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DB 1261 CTCACCGTGGACAAAGAGAGGTGGCAGAGGGGAACTCTTCTCATGCTCCGATGCAT 1320  
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XX XX  
XX AC AAA91074;  
XX AC  
XX XX  
XX DT 05-APR-2001 (first entry)  
XX XX  
XX DE Flt1 receptor fusion protein Flt1D2.Flt1D3:FcDeltaCl(a) coding sequence.  
XX XX  
XX KW Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic;  
XX KW plasma leakage; vascular permeability; IGF Fc region; ss.  
XX XX  
XX OS Unidentified.  
XX OS  
XX XX  
XX PN WO200075319-A1.  
XX XX  
XX PD 14-DEC-2000.  
XX XX  
XX XX 23-MAY-2000; 2000WO-US014142.  
XX XX  
XX PR 08-JUN-1999; 99US-0138133P.  
XX XX





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PH Key Location/Qualifiers
FT CDS 69..1445
/*tag= a
/*product= "FtlD3.FlikD3.FcDELTA1(a)"
XX WO200260489-A1.
XX 08-AUG-2002.
XX 28-JAN-2002; 2002WO-US002466.
XX 31-JAN-2001; 2001US-00773877.
XX (REGE-) REGENERON PHARM INC.
XX Xia Y, Rudge JS, Yancopoulos GD;
XX WPI; 2002-608488/65.
XX P-PSDB; ABP52447.
XX Treating psoriasis and enhancing wound healing in humans comprises the
PT administration of a vascular endothelial cell growth factor (VEGF)
PT antagonist.
XX Example 17; Fig 21A-C; 179pp; English.
XX The present invention describes a method for treating psoriasis and
XX enhancing wound healing in a mammal or a human. The method comprises
XX administering a vascular endothelial cell growth factor (VEGF) antagonist
XX to the mammal or human. A VEGF antagonist has antipsoriatic,
XX antiinflammatory, vulnery, antiasthmatic, antirheumatic, antiarthritic,
XX nephrotropic and ophthalmological activities. The method can be used in
XX treating psoriasis and enhancing wound healing in humans by administering
XX VEGF antagonist. The method is also useful in treating clinical
XX conditions characterised by vascular permeability, oedema or
XX inflammation, such as brain oedema associated with injury, oedema
XX associated with inflammatory disorders (e.g. rheumatoid arthritis),
XX asthma, burns, kidney diseases, or eye disorders such as age-related
XX macular degeneration and diabetic retinopathy. The method may also be
XX used in making the polypeptide to decrease or inhibit plasma leakage and
XX or vascular permeability. The present sequence encodes
XX FtlD3.FlikD3.FcDELTA1(a) which is used in an example from the present
XX invention
SQ Sequence 1453 BP; 398 A; 400 C; 366 G; 289 T; 0 U; 0 Other;
Query Match 96.5%; Score 1328.4; DB 6; Length 1453;
Best Local Similarity 98.6%; Pred. No. 3e-312;
Matches 1367; Conservative 0; Mismatches 1; Indels 18; Gaps 2;
QY 1 ATGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGTGTCTAGCTGTCTGCTTCTC 60
DB |||||||
DB 69 ATGTCAGCTACTGGGACACCGGGGTCCTGCTGTGCGCGTGTCTAGCTGTCTGCTTCTC 128
QY 61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTTCGTAGAGATGTACAGTGAATC 120
DB |||||||
DB 129 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTTCGTAGAGATGTACAGTGAATC 179
QY 121 CCCGAAATTTACACATGACTGAAGGAAGGAGCTGTGATTCCTGCGGGTGTACGTCA 180
DB |||||||
DB 180 CCCGAAATTTACACATGACTGAAGGAAGGAGCTGTGATTCCTGCGGGTGTACGTCA 239
QY 181 CCTAACATCACTGTTACTTTTAAAGTTTCCACTTGACACTTTGATCCCTGATGGAATA 240
DB |||||||
DB 240 CCTAACATCACTGTTACTTTTAAAGTTTCCACTTGACACTTTGATCCCTGATGGAATA 299
QY 241 CGCATATCTGGGACAGTAGAAGGGCTTCATCATATCAATCAATGCAAGTGAAGAAATA 300
DB |||||||
DB 300 CGCATATCTGGGACAGTAGAAGGGCTTCATCATATCAATCAATGCAAGTGAAGAAATA 359
QY 301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCAATTTGTATGAAGCAAACTATCTACA 360
DB |||||||
DB 360 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCAATTTGTATGAAGCAAACTATCTACA 419
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361 CATCGACAAACCAATACAAATCATAGATGTGGTTCTGAGTCCGCTCATGGAATTGAAC 420
420 CATCGACAAACCAATACAAATCATAGATGTGGTTCTGAGTCCGCTCATGGAATTGAAC 479
421 TCTGTTGGAGAAAAGCTTGTCTTAAATTTGTACAGCAAGAACTGAACTAAATGTGGG 480
480 TCTGTTGGAGAAAAGCTTGTCTTAAATTTGTACAGCAAGAACTGAACTAAATGTGGG 539
481 GACTTCAACTGGGAATACCTCTTCGAAGCATCAGCATAAGAACTTTGAAACCCGAGAC 540
540 GACTTCAACTGGGAATACCTCTTCGAAGCATCAGCATAAGAACTTTGAAACCCGAGAC 599
541 CTAATAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGGAGCACCTTAACTATAGAT 600
600 CTAATAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGGAGCACCTTAACTATAGAT 659
601 GTAAACCCGAGTGACCAAGGATTTGTACCTGTGAGCATCCAGTGGGCTGTAGTCAAG 660
660 GTAAACCCGAGTGACCAAGGATTTGTACCTGTGAGCATCCAGTGGGCTGTAGTCAAG 719
661 AAGAACAGCACATTTCTCAGGGTCCATGAAAG-----GACAAAACCTCACATGC 711
720 AAGAACAGCACATTTCTCAGGGTCCATGAAAGGGGCCCGGGCCGACAACTCACATGC 779
712 CCACCGTGGCCAGCACCTGAACTCTCTGGGGGACCGTCAAGTCTTCTCTTCCCCCAAAA 771
780 CCACCGTGGCCAGCACCTGAACTCTCTGGGGGACCGTCAAGTCTTCTCTTCCCCCAAAA 839
772 CCCAAGGACACCTCTATGATCTCCCGGACCCCTGAGGTACATGCGTGTGGTGGAGCG 831
840 CCCAAGGACACCTCTATGATCTCCCGGACCCCTGAGGTACATGCGTGTGGTGGAGCG 899
832 AGCCAGGACACCTCTGAGTCAAGTTCCTGAGTGTGAGCGCGTGGAGGTGCATAAT 891
900 AGCCAGGACACCTCTGAGTCAAGTTCCTGAGTGTGAGCGCGTGGAGGTGCATAAT 959
892 GCCAAGACAAAGCCGCGGAGGAGCAGTACAAACAGCACGCTACCGTGTGGTGGAGCG 951
960 GCCAAGACAAAGCCGCGGAGGAGCAGTACAAACAGCACGCTACCGTGTGGTGGAGCG 1019
952 ACCGTCTGTGACAGGACTGGCTGAAATGGCAAGGATGACAGTGTCAAGTGTCTCAACAA 1011
1020 ACCGTCTGTGACAGGACTGGCTGAAATGGCAAGGATGACAGTGTCAAGTGTCTCAACAA 1079
1012 GCCCTCCAGCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCGGAGACCA 1071
1080 GCCCTCCAGCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCGGAGACCA 1139
1072 CAGGTGTACACCTGTGCCCCCATCTCCCGGATGAGTGCACCAAGAACAGGTGAGCTGACC 1131
1140 CAGGTGTACACCTGTGCCCCCATCTCCCGGATGAGTGCACCAAGAACAGGTGAGCTGACC 1199
1132 TGCCTGGTCAAAAGGCTTCTATCCAGCGACATCCCGTGGAGTGGGAGAGCAATGGGCGAG 1191
1200 TGCCTGGTCAAAAGGCTTCTATCCAGCGACATCCCGTGGAGTGGGAGAGCAATGGGCGAG 1259
1192 CCGGAGAACAACTACAAAGCAGCCCTCCCGTGTGAGTCCCGACCGCTCTTCTTCTCCTC 1251
1260 CCGGAGAACAACTACAAAGCAGCCCTCCCGTGTGAGTCCCGACCGCTCTTCTTCTCCTC 1319
1252 TACAGCAAGCTACCTGTGCAAGAGCAGGTGGCAGCAGGGGAAACGCTTCTCATGTCTCC 1311
1320 TATAGCAAGCTACCTGTGCAAGAGCAGGTGGCAGCAGGGGAAACGCTTCTCATGTCTCC 1379
1312 GTGATCATGAGGCTCTGCACAACTACACGAGAGAGCCTCTCCCTGTCTCCGGGT 1371
1380 GTGATCATGAGGCTCTGCACAACTACACGAGAGAGCCTCTCCCTGTCTCCGGGT 1439
1372 AAATGA 1377
1440 AAATGA 1445
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Db 1431 AATGA 1436

RESULT 6  
ABQ74609  
ID ABQ74609 standard; cDNA; 1444 BP.  
XX AC  
XX ABQ74609;  
XX  
XX 23-OCT-2002 (first entry)  
XX  
XX Modified Flt1 receptor Flt1D2.VEGFR3D3.FcDELTA1(a) nucleotide sequence.  
XX  
XX Human; Flt1; vascular endothelial growth factor; VEGF; VEGF antagonist;  
KW psoriasis; wound healing; Flt1 receptor; antipsoriatic; antiinflammatory;  
KW vulnary; antiasthmatic; antirheumatic; antiarthritic; nephrotropic;  
KW ophthalmological; vascular permeability; oedema; inflammation; asthma;  
KW brain oedema; inflammatory disorder; rheumatoid arthritis; burn;  
KW kidney disease; eye disorder; age-related macular degeneration;  
KW diabetic retinopathy; gene; ss.  
XX  
XX Homo sapiens.  
OS  
OS Synthetic.  
OS  
FH Key Location/Qualifiers  
FT CDS 69..1436  
FT FT /\*tag= a  
FT FT /product= "Flt1D2.VEGFR3D3.FcDELTA1(a) "  
XX  
XX WO200260489-A1.  
XX  
XX 08-AUG-2002.  
XX  
XX 28-JAN-2002; 2002WO-US002466.  
XX  
XX 31-JAN-2001; 2001US-00773977.  
XX  
XX (REG- ) REGENERON PHARM INC.  
XX  
XX Xia Y, Rudge JS, Yancopoulos GD;  
XX  
XX WPI; 2002-608488/65.  
DR P-PSDB; ABP52448.  
XX  
XX Treating psoriasis and enhancing wound healing in humans comprises the  
PT administration of a vascular endothelial cell growth factor (VEGF)  
PT antagonist.  
XX  
XX Example 17; Fig 22A-C; 179pp; English.  
XX  
XX The present invention describes a method for treating psoriasis and  
CC enhancing wound healing in a mammal or a human. The method comprises  
CC administering a vascular endothelial cell growth factor (VEGF) antagonist  
CC to the mammal or human. A VEGF antagonist has antipsoriatic,  
CC antiinflammatory, vulnary, antiasthmatic, antirheumatic, antiarthritic,  
CC nephrotropic and ophthalmological activities. The method can be used in  
CC treating psoriasis and enhancing wound healing in humans by administering  
CC VEGF antagonist. The method is also useful in treating clinical  
CC conditions characterised by vascular permeability, oedema or  
CC inflammation, such as brain oedema associated with injury, oedema  
CC associated with inflammatory disorders (e.g. rheumatoid arthritis),  
CC asthma, burns, kidney diseases, or eye disorders such as age-related  
CC macular degeneration and diabetic retinopathy. The method may also be  
CC used in making the polypeptide to decrease or inhibit plasma leakage and  
CC or vascular permeability. The present sequence encodes  
CC Flt1D2.VEGFR3D3.FcDELTA1(a) which is used in an example from the present  
XX invention  
XX  
SQ Sequence 1444 BP; 371 A; 426 C; 380 G; 267 T; 0 U; 0 Other;  
Query Match 76.2%; Score 1049.2; DB 6; Length 1444;  
Best Local Similarity 86.7%; Pred. No. 1.8e-244;  
Matches 1201; Conservative 0; Mismatches 158; Indels 27; Gaps 3;

QY 1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGCGCGCTGCTCAGCTGTCTCTTCTC 60  
DB 69 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGCGCGCTGCTCAGCTGTCTCTTCTC 128  
QY 61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTTCGTAGAGATGTACAGTGAATC 120  
DB 129 ACAGGATCTAGTTCCGGA-----GGTAGACCTTTTCGTAGAGATGTACAGTGAATC 179  
QY 121 CCGAAATATTACACATGACTGAAGGAGGAGCTCGTCAATCCCTCCGGTTACGTCA 180  
DB 180 CCGAAATATTACACATGACTGAAGGAGGAGCTCGTCAATCCCTCCGGTTACGTCA 239  
QY 181 CCTAACATCACTGTCTTTTAAAGAGTTTCCACTTGACACTTTTGATCCCTGTATGGAATA 240  
DB 240 CCTAACATCACTGTCTTTTAAAGAGTTTCCACTTGACACTTTTGATCCCTGTATGGAATA 299  
QY 241 CGCATATCTGGGACAGTAGAAGGGCTTCATCATATCAATCAATGCAAGCTACAAAGAATA 300  
DB 300 CGCATATCTGGGACAGTAGAAGGGCTTCATCATATCAATCAATGCAAGCTACAAAGAATA 359  
QY 301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAGACAAACTATCTCACA 360  
DB 360 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAGACAAACTATCTCACA 419  
QY 361 CATCGACAAACCAATACATATAGATGTGGTTCTGAGTCCGCTCATGGAATTTGAACATA 420  
DB 420 CATCGACAAACCAATACATATAGATGTGGTTCTGAGTCCGCTCATGGAATTTGAACATA 479  
QY 421 TCTGTTGGAGAAAGCTTGTCTTAAATTTGATAGAGCAAGAACTGAACTAAATGTGGGATT 480  
DB 480 CTGGTAGGGGAGAGCTGTCTCAACTGCACCGCTGTGGGCTAGTTTAACTCAGGTGTC 539  
QY 481 GACTTCAACTGGGAATACCTCTTTCGAGCATCAGCATAGAACTTTGTAAACCGAGAC 540  
DB 540 ACCTTTGACTGGGACTACCCAGGAGCAGGAGCGGGTAAAGTGGGTGCCCGAGCGA 599  
QY 541 CTAAAAAACCAGTCTGGGAGTGAGATGAAGAAATTTTGGAGCACCTTTAACTATAGATGGT 600  
DB 600 CGCTCCACACAGACCCACACAG-----AACTCTCAGCATCTCGACCATCCACAC 650  
QY 601 GTAAACCGGAGTGACCAAGGATTTGACACTGTGTCAGCATCTCAGTGGGCTGATGACCAAG 660  
DB 651 GTCAGGCAGCACGACCTGGGCTGTATGTGCAAGGCCAACCAACGGCATCCAGCGATTT 710  
QY 661 AAGAACAGCACATTTCTCAGGGTCCATGAAA-----GGACAAACTCACACATGC 711  
DB 711 CCGGAGAGCACCGAGGTCTATTGTGCATGAAAATGGCCCGGGCGCAAAACTCACACATGC 770  
QY 712 CCACCGTGGCCAGCACCTGAACTCCTGGGGGACCGTCAGTCTTCTTCCCCCCTCAAAA 771  
DB 771 CCACCGTGGCCAGCACCTGAACTCCTGGGGGACCGTCAGTCTTCTTCCCCCCTCAAAA 830  
QY 772 CCCAAGGACACCTCATATGATCTCCCGGACCCCTGAGGTACATCGGTGGTGGAGCGTG 831  
DB 831 CCCAAGGACACCTCATATGATCTCCCGGACCCCTGAGGTACATCGGTGGTGGAGCGTG 890  
QY 832 AGCCAGGAGACCTCAGGTCAAGTTCACTGTGAGTGGACCGCGTGGAGGTGCATAAT 891  
DB 891 AGCCAGGAGACCTCAGGTCAAGTTCACTGTGAGTGGACCGCGTGGAGGTGCATAAT 950  
QY 892 GCCAAGACAAAGCGGGGAGGAGCAGTACAAACAGCACGTCACGTGTGGTGGAGGTCTC 951  
DB 951 GCCAAGACAAAGCGGGGAGGAGCAGTACAAACAGCACGTCACGTGTGGTGGAGGTCTC 1010  
QY 952 ACCGTCTGCACAGGACTGGTGAATTTGCAAGAGGTACAAAGTGCAGAGGTCTCCACAAA 1011  
DB 1011 ACCGTCTGCACAGGACTGGTGAATTTGCAAGAGGTACAAAGTGCAGAGGTCTCCACAAA 1070  
QY 1012 GCCCTCCAGCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCGAGCCCGGAGACCA 1071  
DB 1071 GCCCTCCAGCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCGAGCCCGGAGACCA 1130

QY 1072 CAGGTGTACACCTGCCCATCCCGGATAGCTGACCAAGAACAGGTTCAGCCTGACC 1131  
Db |||||  
QY 1131 CAGGTGTACACCTGCCCATCCCGGATAGCTGACCAAGAACAGGTTCAGCCTGACC 1190  
Db |||||  
QY 1132 TGCTGTGTCAGAGCTTCTATCCAGCGACATCGCGTGGAGTGGGAGAGCAATGGGCAG 1191  
Db |||||  
QY 1191 TGCTGTGTCAGAGCTTCTATCCAGCGACATCGCGTGGAGTGGGAGAGCAATGGGCAG 1250  
QY 1192 CCGGAGAACAACTACAAAGACACGCTCCGCTGCTGGACTCCGACGGCTCTTCTTCCTC 1251  
Db |||||  
QY 1251 CCGGAGAACAACTACAAAGACACGCTCCGCTGCTGGACTCCGACGGCTCTTCTTCCTC 1310  
QY 1252 TACAGCAAGCTCACCGTGGACAGACAGCTGGCAGCAGGGAACTCTTCTCATGCTCC 1311  
Db |||||  
QY 1311 TATAGCAAGCTCACCGTGGACAGACAGCTGGCAGCAGGGAACTCTTCTCATGCTCC 1370  
QY 1312 GTGATGATGAGGCTCTGCACAACTACACGACAGAGGCTCTCCCTGTCTCCGGGT 1371  
Db |||||  
QY 1371 GTGATGATGAGGCTCTGCACAACTACACGACAGAGGCTCTCCCTGTCTCCGGGT 1430  
QY 1372 AATGA 1377  
Db |||||  
QY 1431 AATGA 1436

RESULT 7  
ID AAA91071 standard; DNA; 1359 BP.  
XX  
AC AAA91071;  
XX  
DT 05-APR-2001 (first entry)  
XX  
DE Ftl1 receptor fusion protein Mut2:Ftl1(2-3deltaB)-Fc coding sequence.  
XX  
DE Ftl1 receptor; fusion protein; chimeric protein; pharmacokinetic;  
KW plasma leakage; vascular permeability; IgG Fc region; ss.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT 1. .1359  
CDS /tag= a  
FT /product= "Ftl1(2-3deltaB)-Fc"  
XX  
PN WO200075319-A1.  
XX  
PD 14-DEC-2000.  
XX  
PF 23-MAY-2000; 2000WO-US014142.  
XX  
PR 08-JUN-1999; 99US-0138133P.  
XX  
PA (REG-) REGENERON PHARM INC.  
XX  
PI Papadopoulos NJ, Davis S, Yancopoulos GD;  
XX  
DR WPI; 2001-071076/08.  
DR P-PSDB; AAY97591.  
XX

XX Nucleic acid molecule encoding mammalian phospholipid transfer protein,  
PT and its fragments, useful for diagnosis, evaluation, and treatment of  
PT diseases associated with the gene expression and for producing model  
PT systems.  
XX  
PS Claim 9; Fig 14; 159pp; English.  
XX  
CC This sequence encodes a fusion protein of the invention between the Ftl1  
CC receptor and the Fc region of IgG. The specification relates to modified  
CC chimeric polypeptides with improved pharmacokinetics. The modified  
CC chimeric polypeptides are preferably Ftl1 receptor polypeptides that have  
CC been modified to improve their pharmacokinetic profile. The polypeptides  
CC can be used to decrease or inhibit plasma leakage and/or vascular

CC permeability in a mammal  
XX Sequence 1359 BP; 381 A; 388 C; 314 G; 276 T; 0 U; 0 Other;  
SQ  
Query Match 75.5%; Score 1039; DB 5; Length 1359;  
Best Local Similarity 86.3%; Pred. No. 5.3e-242;  
Matches 1189; Conservative 0; Mismatches 170; Indels 18; Gaps 3;  
QY 1 ATGGTCAGCTACTGGGACACCGGGTCTGCTGTGGCGCTGCTAGCTGTCTGCTTCTC 60  
Db |||||  
QY 1 ATGGTCAGCTACTGGGACACCGGGTCTGCTGTGGCGCTGCTAGCTGTCTGCTTCTC 60  
Db |||||  
QY 61 ACAGATCTAGTTCGGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAATC 120  
Db |||||  
QY 61 ACAGATCTAGTTCGGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAATC 111  
Db |||||  
QY 121 CCCGAAATTTATACATGATCTGAAGGAGGAGCTCGTCAATTCCTGCGGGTTACGTCA 180  
Db |||||  
QY 112 CCCGAAATTTATACATGATCTGAAGGAGGAGCTCGTCAATTCCTGCGGGTTACGTCA 171  
Db |||||  
QY 181 CCTAATCATCTGTTACTTTTAAAAAGTTTCCACTTGACACTTTGATCCTCGATGAAAA 240  
Db |||||  
QY 172 CCTAATCATCTGTTACTTTTAAAAAGTTTCCACTTGACACTTTGATCCTCGATGAAAA 231  
Db |||||  
QY 241 CGCATAATCTGGGACAGTAGAAGGCTTTCATCATATCAATCAAAATGCAACGTACAAAGAA 300  
Db |||||  
QY 232 CGCATAATCTGGGACAGTAGAAGGCTTTCATCATATCAATCAAAATGCAACGTACAAAGAA 291  
Db |||||  
QY 301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCAATTTGTATAAGCAAACTATCTCA 360  
Db |||||  
QY 292 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCAATTTGTATAAGCAAACTATCTCA 351  
Db |||||  
QY 361 CATCGACAAACCAATACATATAGATGTGTTCTGAGTCCGCTCATCGAATTTGAACTA 420  
Db |||||  
QY 352 CATCGACAAACCAATACATATAGATGTGTTCTGAGTCCGCTCATCGAATTTGAACTA 411  
Db |||||  
QY 421 TCTGTTGGAGAAAGCTTCTTAAATTTGACAGCAAGAACTGAACTAAATGTGGGAT 480  
Db |||||  
QY 412 CTTAGAGGCCATCTCTTGTCTCAATTTGATCTGCTACCTCCCTTGAACAGGAGTT 471  
Db |||||  
QY 481 GACTTCAACTGGGAATACCTTCTTGAAGCATACGATCAAGAACTTGTAAACCGAGAC 540  
Db |||||  
QY 472 CAAATGACCTGGAGTTACCTCTGATGAAATTTGACCAAGCAATTCCTCATCCCAATATTC 531  
Db |||||  
QY 541 CTAATAAACCCAGTCTGGGAGTGAAGAAATTTTGGAGCACTTAACTATAGATGT 600  
Db |||||  
QY 532 TACAGTGTCTTACTATTGACAAATGACAAAGCAAAAGAGACTTTTATATCTGTCT 591  
Db |||||  
QY 601 GTAAACCCGGAGTGACCAAGGATTTGACACCTCTGAGCATCCAGTGGGCTGATGACCAAG 660  
Db |||||  
QY 592 GTAAACCCGGAGTGACCAAGGATTTGACACCTCTGAGCATCCAGTGGGCTGATGACCAAG 642  
Db |||||  
QY 661 AAGAAACAGCACATTTGTCAGGGTCCATGAAAGGAGCAAAACTCACATGCCACCGTGC 720  
Db |||||  
QY 643 GATAAAGCAGGCGCGGGAGGCCAAAATCTTGTGACAAAACCTCACATGCCACCGTGC 702  
Db |||||  
QY 721 CCAGCACTGAACTCTCTGGGGGACCGTCAAGTCTTCTCTTCCCGCAAAACCCCAAGGAC 780  
Db |||||  
QY 703 CCAGCACTGAACTCTCTGGGGGACCGTCAAGTCTTCTCTTCCCGCAAAACCCCAAGGAC 762  
Db |||||  
QY 781 ACCCTCATGATCTCCGGGACCCCTGAGGTTCACATCGTGGTGGTGGAGCTGAGCCACGAA 840  
Db |||||  
QY 763 ACCCTCATGATCTCCGGGACCCCTGAGGTTCACATCGTGGTGGTGGAGCTGAGCCACGAA 822  
Db |||||  
QY 841 GACCTTGAGGTCAAGTTCACTGTAAGTGAAGGAGGAGTGCATTAATGCCAAGACA 900  
Db |||||  
QY 823 GACCTTGAGGTCAAGTTCACTGTAAGTGAAGGAGGAGTGCATTAATGCCAAGACA 882  
Db |||||  
QY 901 AAGCCGGGAGGAGGAGTGAACAGCAGTACCGTGTGCTGAGCGTCTCTACCGTCTCG 960  
Db |||||  
QY 883 AAGCCGGGAGGAGGAGTGAACAGCAGTACCGTGTGCTGAGCGTCTCTACCGTCTCG 942  
Db |||||  
QY 961 CACCAGGACTGGCTGAAATGGCAAGGAGTACAAGTGAAGGTCTCCAAACAAAGCCCTCCCA 1020  
Db |||||

Db 943 CACGAGGACTGGTGAATGCAAGGAGTACAAGTGAAGTCTCCAAACAAAGCCCTCCCA 1002  
QY 1021 GCCCCTATCGAGAAACCATCTCCAAAGCCAAAGGCGAGCCCGAGAACACACAGGTGTAC 1080  
Db 1003 GCCCCTATCGAGAAACCATCTCCAAAGCCAAAGGCGAGCCCGAGAACACACAGGTGTAC 1062  
QY 1081 ACCCTGCCCTATCCCGGATGAGCTGACCAAGAACACAGGTGAGCTGACCTGCTGGTC 1140  
Db 1063 ACCCTGCCCTATCCCGGATGAGCTGACCAAGAACACAGGTGAGCTGACCTGCTGGTC 1122  
QY 1141 AAGGCTTCTATCCAGCGATCGCGGTGAGTGGAGAGCAATGGGCGAGCCGAGAAC 1200  
Db 1123 AAGGCTTCTATCCAGCGATCGCGGTGAGTGGAGAGCAATGGGCGAGCCGAGAAC 1182  
QY 1201 AACTCAAGACACCGCTCCCGTGTGACTCCGAGCGCTCTTCTTCTCTACAGCAAG 1260  
Db 1183 AACTCAAGACACCGCTCCCGTGTGACTCCGAGCGCTCTTCTTCTCTACAGCAAG 1242  
QY 1261 CTCACCGTGGACCAAGAGCGAGTGGCGAGCGAGGGAACGTCTTCTCATGCTCCGTGATGCAT 1320  
Db 1243 CTCACCGTGGACCAAGAGCGAGTGGCGAGCGAGGGAACGTCTTCTCATGCTCCGTGATGCAT 1302  
QY 1321 GAGGCTCTGCACCAACCACTACACGCGAGAGAGCTCTCCCTGTCTCCGGTAAATGA 1377  
Db 1303 GAGGCTCTGCACCAACCACTACACGCGAGAGAGCTCTCCCTGTCTCCGGTAAATGA 1359

RESULT 8  
ABQ74605  
ID ABQ74605 standard; cDNA; 1359 BP.  
XX ABQ74605;  
XX  
XX 23-OCT-2002 (first entry)  
DT  
XX  
DE Mutation 2 Flt1(2-3 delta B)-Fc nucleotide sequence.  
XX Human; Flt1; vascular endothelial growth factor; VEGF; VEGF antagonist;  
KW psoriasis; wound healing; Flt1 receptor; antipsoriatic; antiinflammatory;  
KW vulnery; antiasthmatic; antirheumatic; antiarthritic; nephrotropic;  
KW ophthalmological; vascular permeability; oedema; inflammation; asthma;  
KW brain oedema; inflammatory disorder; rheumatoid arthritis; burn;  
KW kidney disease; eye disorder; age-related macular degeneration;  
KW diabetic retinopathy; gene; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.

Key Location/Qualifiers  
FH 1. .1359  
CDS /\*tag= a  
FT /product= "Mut2:Flt1(2-3 delta B)-Fc protein"

XX WO200260489-A1.  
PN  
XX  
XX 08-AUG-2002.  
XX  
XX 28-JAN-2002; 2002WO-US002466.  
PF  
XX  
XX 31-JAN-2001; 2001US-00773877.  
PR  
XX (REG- ) REGENERON PHARM INC.  
XX  
XX Xia Y, Rudge JS, Yancopoulos GD;  
PI  
XX WPI; 2002-608488/65.  
XX  
DR P-PSDB; ABP52444.  
DR  
XX  
XX Treating psoriasis and enhancing wound healing in humans comprises the  
PT administration of a vascular endothelial cell growth factor (VEGF)  
PT antagonist.  
XX

Example 12; Fig 14A-C; 179pp; English.

PS The present invention describes a method for treating psoriasis and  
XX enhancing wound healing in a mammal or a human. The method comprises  
CC administering a vascular endothelial cell growth factor (VEGF) antagonist  
CC to the mammal or human. A VEGF antagonist has antipsoriatic,  
CC antiinflammatory, vulnerary, antiasthmatic, antirheumatic, antiarthritic,  
CC nephrotropic and ophthalmological activities. The method can be used in  
CC treating psoriasis and enhancing wound healing in humans by administering  
CC VEGF antagonist. The method is also useful in treating clinical  
CC conditions characterised by vascular permeability, oedema or  
CC inflammation, such as brain oedema associated with injury, oedema  
CC associated with inflammatory disorders (e.g. rheumatoid arthritis),  
CC asthma, burns, kidney diseases, or eye disorders such as age-related  
CC macular degeneration and diabetic retinopathy. The method may also be  
CC used in making the polypeptide to decrease or inhibit plasma leakage and  
CC or vascular permeability. The present sequence encodes Mut2:Flt1(2-3  
CC delta B)-Fc which is used in an example from the present invention  
XX

SQ Sequence 1359 BP; 381 A; 388 C; 314 G; 276 T; 0 U; 0 Other;

Query Match 75.5%; Score 1039; DB 6; Length 1359;  
Best Local Similarity 86.3%; Pred. No. 5.3e-242;  
Matches 1189; Conservative 0; Mismatches 170; Indels 18; Gaps 3;

QY 1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGGCGCTGTCTGCTGCTGCTCTC 60  
Db 1 ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGTGGCGCTGTCTGCTGCTGCTCTC 60  
QY 61 ACAGGATCTAGTTCGGGAAGTGNATCCGGTAGACCTTTCTGTAGAGATGTACAGTGAATC 120  
Db 61 ACAGGATCTAGTTCGGGAAGTGNATCCGGTAGACCTTTCTGTAGAGATGTACAGTGAATC 111  
QY 121 CCGGAATTTATACACATGACTGAAGGAGGAGCTCGTCAATCCCTCCCGGGTTACGTCA 180  
Db 112 CCGGAATTTATACACATGACTGAAGGAGGAGCTCGTCAATCCCTCCCGGGTTACGTCA 171  
QY 181 CCTAACATCACTGTTACTTTTAAAAAGTTTCCACTTGACACTTTGATCCCTGATGAAAA 240  
Db 172 CCTAACATCACTGTTACTTTTAAAAAGTTTCCACTTGACACTTTGATCCCTGATGAAAA 231  
QY 241 CGCATTAATCTGGGACAGTGAAGGCTTCATCATATCAAAATCAACGTAACAAAGAAATA 300  
Db 232 CGCATTAATCTGGGACAGTGAAGGCTTCATCATATCAAAATCAACGTAACAAAGAAATA 291  
QY 301 GGGCTTCTGACCTGTGAAGCAAGTCAATGGGCTTTGTATTAAGCAAACTATCTCACA 360  
Db 292 GGGCTTCTGACCTGTGAAGCAAGTCAATGGGCTTTGTATTAAGCAAACTATCTCACA 351  
QY 361 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGCTCATGGAATTTGAACATA 420  
Db 352 CATCGACAAACCAATACAATCATAGATGTGGTTCTGAGTCCGCTCATGGAATTTGAACATA 411  
QY 421 TCTGTTGGAGAAAAGCTTGTCTTAAATTTGACAGCAAGAACTGAACTAAATGTGGGATT 480  
Db 412 CTTAGAGGCCATACCTCTTGTCTCAATTTGTCTACCACTCCCTTGAACAGAGAGTT 471  
QY 481 GACTTCAACTGGGAATACCTCTTTCGAGAGCATCAGCATAGAAGAACTGTAAACCCGAGAC 540  
Db 472 CAAATGACCTGGAGTTACCTCTGATGAAATTTGACAAAGCAATTTCCCATGCCAATATTC 531  
QY 541 CTAAAAAACCCAGTCTGGGAGTGAGATGAAGAAAATTTTGGAGCACCTTAACTATAGATGGT 600  
Db 532 TACAGTGTCTTACTATTGACAAAATGCAGAACAAAGACAAAGACTTTATATCTTGTCTGT 591  
QY 601 GTAAACCCGAGTGACCAAGATTTGTACACTGTGACAGCATTCAGTGGGCTGTGATGACCAAG 660  
Db 592 GTAAACCCGAGTGACCAAGATTTGTACACTGTGACAGCATTCAGTGGGCTGTGATGACCAAG 642  
QY 661 AAGAACAGACATTTGTCTAGGGTCCATGAAGAGCAAAACTCACACATGCCACCGTGC 720  
Db 643 GATAAAGAGCGCCCGGGCGAGCCCAAACTCTTGTGTGACAAAACCTCACACATGCCACCGTGC 702

Qy	721	CCAGC	ACTGAACTCTCTGGGGGACCGT	AGTCTTCTCTTCCCCCAAAACCAAGGAC	780
Db	703	CCAGC	ACTGAACTCTCTGGGGGACCGT	AGTCTTCTCTTCCCCCAAAACCAAGGAC	762
Qy	781	ACCCT	ATGATCTCCCGGACCCCT	AGGTGACATGCGTGGTGGGACGTGAGCCACGAA	840
Db	763	ACCCT	ATGATCTCCCGGACCCCT	AGGTGACATGCGTGGTGGGACGTGAGCCACGAA	822
Qy	841	GACCT	GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCAATAATGCCAAGACA	900	
Db	823	GACCT	GAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCAATAATGCCAAGACA	882	
Qy	901	AAGCC	GGGAGGAGCAGTACAACAGCAGCATGTCGGTGTGTGTCAGCGTCTCTCACGTCCTG	960	
Db	883	AAGCC	GGGAGGAGCAGTACAACAGCAGCATGTCGGTGTGTGTCAGCGTCTCTCACGTCCTG	942	
Qy	961	CACCAG	ACTGGCTGAATGGCAAGGAGTCAAAAGTGCAGAGTCTCCAAACAAGGCCCTCCCA	1020	
Db	943	CACCAG	ACTGGCTGAATGGCAAGGAGTCAAAAGTGCAGAGTCTCCAAACAAGGCCCTCCCA	1002	
Qy	1021	GCCCC	CATCGAGAAAAACATCTCCAAAGCCAAAGGGCAGCCCGCAGAGAACACACAGGTGTAC	1080	
Db	1003	GCCCC	CATCGAGAAAAACATCTCCAAAGCCAAAGGGCAGCCCGCAGAGAACACACAGGTGTAC	1062	
Qy	1081	ACCTG	CCCCCATCCCGGGATGACTGACCAAGAACACAGGTCAAGCTGACCTGCCTGGTC	1140	
Db	1063	ACCTG	CCCCCATCCCGGGATGACTGACCAAGAACACAGGTCAAGCTGACCTGCCTGGTC	1122	
Qy	1141	AAAGG	CTTCTATCCACGCGCATCGCCGTGGAGTGGGAGAGCAATGGCAGCCGGAGAAC	1200	
Db	1123	AAAGG	CTTCTATCCACGCGCATCGCCGTGGAGTGGGAGAGCAATGGCAGCCGGAGAAC	1182	
Qy	1201	AACTA	GAAGACCAAGCTCCCGTGTGACTCCGACGGCTCTTCTTCTCTCTACAGCAAG	1260	
Db	1183	AACTA	GAAGACCAAGCTCCCGTGTGACTCCGACGGCTCTTCTTCTCTCTACAGCAAG	1242	
Qy	1261	CTCAC	CGTGGACAAGACGAGTGGCAGCGGGAAACGTCTTCTCATGCTCCGTGATGCAT	1320	
Db	1243	CTCAC	CGTGGACAAGACGAGTGGCAGCGGGAAACGTCTTCTCATGCTCCGTGATGCAT	1302	
Qy	1321	GAGG	CTTGCAACCAACTACACGCAAGAGCGCTCTCCCTGTGCTCCGGTAAATGA	1377	
Db	1303	GAGG	CTTGCAACCAACTACACGCAAGAGCGCTCTCCCTGTGCTCCGGTAAATGA	1359	

RESULT	9
AAA91072	
ID	AAA91072 standard; DNA; 1389 BP.
XX	
AC	AAA91072;
XX	
DT	05-APR-2001 (first entry)
XX	
Ft1l	receptor fusion protein Mut3:Ft1l(2-3)-Fc coding sequence.
DE	
XX	
KW	Ft1l receptor; fusion protein; chimeric protein; pharmacokinetic; plasma leakage; vascular permeability; IgG Fc region; ss.
XX	
OS	Unidentified.
XX	
Key	Location/Qualifiers
CDS	1..1389
FT	/*tag= a
FT	/product= "Ft1l(2-3)-Fc"
PX	
PN	WO200075319-Al.
XX	
PD	14-DEC-2000.
PP	
Pf	23-MAY-2000; 2000WO-US014142.
PR	
PJ	08-JUN-1999; 99US-0138133P.
XX	





Db 352 CATCGACAAACCAATACATCATAGATGTCCAAATGAAGCACACCGCCAGTCAATTA 411  
Qy 421 TCTGTTGGAGAAAGCTTGTCTTAAATGTGTACAGCAAGAACTGAATAATGTGGGATT 480  
Db 412 CTTAGAGGCCATACTCTGTGCTCAATGTGTACTGTACCCTCCCTTGAACACGAGATT 471  
Qy 481 GACTTCAACTGGGAATACCTTCTTTCGAAGCATCAGCAATGAAGAACTTGAACCGAGAC 540  
Db 472 CAAATGACCTGGAGTTACCTCT-----GATGAAAAAATAAGAGAGCTTCCGTGAAGCGA 525  
Qy 541 CTAAMAAACCCAGTCTGGGAGTGAAGTGAAGAAATTTTGAGCACCTTAACTACTAGATGTT 600  
Db 526 CGAATTGACCAAGCAATTTCCCATGCCAATATCTACAGTGTCTTACTATTGACAA 585  
Qy 601 GTAAACCCGGAGTGACCAAGATTTGTACACTGTGCAGCATCCAGTGGGCTGTGACCAAG 660  
Db 586 ATGCAGAAACAAAGACAAAGGACTTTATACTTGTGTTAAGGAGTGGACCATCATTTCAA 645  
Qy 661 AAGAACAGCACATTTTGTCAAGGTCCATGAANA-----G 693  
Db 646 TCTGTTAACACCTTCAGTGCATATATATGATGAAGCAGGCCCGGGCGAGCCCAAAATCTTGT 705  
Qy 694 GACAAAACTCACATATGCCACCGTCCCGCAGCACCTGAACTCTCTGGGGGACCGTCAAGTC 753  
Db 706 GACAAAACTCACATATGCCACCGTCCCGCAGCACCTGAACTCTCTGGGGGACCGTCAAGTC 765  
Qy 754 TTCCTCTTCCCGCCAAAACCCAAAGGACACCTCATGATCTCCCGGACCCCTGAGGTCACA 813  
Db 766 TTCCTCTTCCCGCCAAAACCCAAAGGACACCTCATGATCTCCCGGACCCCTGAGGTCACA 825  
Qy 814 TCGGTGGTGGTGGACGTGAGCCACGAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGAC 873  
Db 826 TGGGTGGTGGTGGACGTGAGCCACGAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGAC 885  
Qy 874 GCGGTGGAGGTGCATAATGCCAAGACAAAGCCCGGGAGGAGCAGTACAAACAGCAGTAC 933  
Db 886 GCGGTGGAGGTGCATAATGCCAAGACAAAGCCCGGGAGGAGCAGTACAAACAGCAGTAC 945  
Qy 934 CGTGTGGTCAGCGTCTCAACCGTCTGTGCACAGGACTGTGCTGAATGGCAAGGATACAAG 993  
Db 946 CGTGTGGTCAGCGTCTCAACCGTCTGTGCACAGGACTGTGCTGAATGGCAAGGATACAAG 1005  
Qy 994 TGCAGGTCTTCAACAAAGCCCTCCAGCCCGCCCATCGAAGAACCATCTCCAAAGCCAAA 1053  
Db 1006 TGCAGGTCTTCAACAAAGCCCTCCAGCCCGCCCATCGAAGAACCATCTCCAAAGCCAAA 1065  
Qy 1054 GGGCAGCCCGGAGAACCAAGGTGTACACCCCTGCCCGCCCATCCCGGATGAGCTGACCAAG 1113  
Db 1066 GGGCAGCCCGGAGAACCAAGGTGTACACCCCTGCCCGCCCATCCCGGATGAGCTGACCAAG 1125  
Qy 1114 AACCAGGTGAGCTGACCTGCTGTGFTCAAGGCTTCTATCCAGCGACATCCCGTGGAG 1173  
Db 1126 AACCAGGTGAGCTGACCTGCTGTGFTCAAGGCTTCTATCCAGCGACATCCCGTGGAG 1185  
Qy 1174 TGGGAGCAATGGGAGCGGAGAACACTACAGACCAAGCCCTCCCGTGTGACTCC 1233  
Db 1186 TGGGAGCAATGGGAGCGGAGAACACTACAGACCAAGCCCTCCCGTGTGACTCC 1245  
Qy 1234 GACGGTCTCTTCTTCTACAGCAAGCTCACCGTGGACAAAGAGCAGGTGGCAGAGGGG 1293  
Db 1246 GACGGTCTCTTCTTCTACAGCAAGCTCACCGTGGACAAAGAGCAGGTGGCAGAGGGG 1305  
Qy 1294 AAGCTCTTCTATGCTCCGTGTATGATGAGGCTTGTGCAAAACCACTACACGAGAGAGC 1353  
Db 1306 AAGCTCTTCTATGCTCCGTGTATGATGAGGCTTGTGCAAAACCACTACACGAGAGAGC 1365  
Qy 1354 CTCTCCCTCTCTCCGGTAAATGA 1377  
Db 1366 CTCTCCCTCTCTCCGGTAAATGA 1389

AAA91070  
ID AAA91070 standard; DNA; 1674 BP.  
XX  
AC AAA91070;  
XX  
DT 05-APR-2001 (first entry)  
XX  
DE Flt1 receptor fusion protein Mutl:Flt1(1-3deltaB)-Fc coding sequence.  
XX  
KW Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic;  
plasma leakage; vascular permeability; IgG Fc region; ss.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..1674  
FT /tag= a  
FT /product= "Flt1(1-3deltaB)-Fc"  
XX  
PN WO200075319-A1.  
XX  
PD 14-DEC-2000.  
XX  
PF 23-MAY-2000; 2000WO-US014142.  
XX  
PR 08-JUN-1999; 99US-0138133P.  
XX  
PA (REG-) REGENERON PHARM INC.  
XX  
PI Papadopoulos NJ, Davis S, Yancopoulos GD;  
XX  
DR WPI; 2001-071076/08.  
DR P-PSDB; AAY97590.  
XX  
PT Nucleic acid molecule encoding mammalian phospholipid transfer protein,  
and its fragments, useful for diagnosis, evaluation, and treatment of  
diseases associated with the gene expression and for producing model  
systems.  
XX  
PS Claim 9; Fig 13; 159pp; English.  
XX  
CC This sequence encodes a fusion protein of the invention between the Flt1  
receptor and the Fc region of IgG. The specification relates to modified  
chimeric polypeptides with improved pharmacokinetics. The modified  
chimeric polypeptides are preferably Flt1 receptor polypeptides that have  
been modified to improve their pharmacokinetic profile. The polypeptides  
can be used to decrease or inhibit plasma leakage and/or vascular  
permeability in a mammal  
XX  
SQ Sequence 1674 BP; 495 A; 455 C; 378 G; 346 T; 0 U; 0 Other;  
  
Query Match 71.7%; Score 987.4; DB 5; Length 1674;  
Best Local Similarity 86.1%; Pred. No. 1.9e-229;  
Matches 1119; Conservative 0; Mismatches 171; Indels 9; Gaps 2;  
  
Qy 79 ACTGTATCCGTAGACCTTTCGTAGAGATGTACAGTGAATCCCGAATTTATACACATG 138  
Db 385 AGTGATACAGGTAGACCTTTCGTAGAGATGTACAGTGAATCCCGAATTTATACACATG 444  
Qy 139 ACTGAAGGAAGGAGCTCGTCAATCCCTCCCGGTTACGTCACTCACTTACTTACT 198  
Db 445 ACTGAAGGAAGGAGCTCGTCAATCCCTCCCGGTTACGTCACTTACTTACT 504  
Qy 199 TTAATAAAAGTTTCCACTTGACACTTTTGATCCCTGATGGAACCGCATATCTGGGACGT 258  
Db 505 TTAATAAAAGTTTCCACTTGACACTTTTGATCCCTGATGGAACCGCATATCTGGGACGT 564  
Qy 259 AGAAAGGGCTTCATCATATCAATCCAGGTACAAAGAAATAGGGCTTCTGACCTGTGA 318  
Db 565 AGAAAGGGCTTCATCATATCAATCCAGGTACAAAGAAATAGGGCTTCTGACCTGTGA 624  
Qy 319 GCAACAGTCAATGGGCATTTGTATAGACAAACTATCTCACACATCGACAAACCAATACA 378

Db 625 GCAACAGTCAATGGCATTGTTATAGACAAACATATCTCACATCGACAAACCAATACA 694  
QY 379 ATCATAGATGCTGCTCTGAGTCCGCTCATGGAAATGGAACATATCTGTGGAGAAAGCTT 438  
Db 685 ATCATAGATGCTCAATAGCAACACACGCCAGTCAATATTCTTAGAGCCCATCTCTT 744  
QY 439 GTCTTAATTTGTACAGCAAGAACTGAACCTAAATGTGGGATTGACTTCAACTCGGAATAC 498  
Db 745 GTCTCAATTTGTACTGCTACCACTCCCTTGAACACAGAGATTCAATGACCTGGAGTTAC 804  
QY 499 CTTCTTCGAGCATCAGCATAGAAACTGTGTAAACCGAGACCTAAACCCAGTCTGGG 558  
Db 805 CCTGATGAATTCACCAAGCAATCCCATGCCAACATATTCACAGTGTCTTACTATT 864  
QY 559 AGTGAGATGAAGAAATTTTGTAGCACCCTTAACCTATAGATGGTGTAAACCGGAGTGACCA 618  
Db 865 GACAAATGCAAGAAACAAAGGACTTTATCTTGTCTGTAA---GGAGTGGACCA 921  
QY 619 GGATTGTACACCTGTGAGCATCCAGTGGGCTGATGACCAAGAAAGACACATTTGTC 678  
Db 922 TCATTCAAAATCTGTTAACACCTC-----AGTGCATATATATGATAAAGCAGGCCCGGC 975  
QY 679 AGGTCCTGAAAAGGACAAACTCACATGCCACCGTCCCGACGACCTGAACCTCTG 738  
Db 976 GAGCCCAAAATCTTGTGACAAACTCACATGCCACCGTCCCGACGACCTGAACCTCTG 1035  
QY 739 GGGGGACCGTCAGTCTCTCTCTTCCCGCCAAACCCAAAGGACACCTCATGATCTCCCG 798  
Db 1036 GGGGGACCGTCAGTCTCTCTCTTCCCGCCAAACCCAAAGGACACCTCATGATCTCCCG 1095  
QY 799 ACCCTGAGGTCAATGCGTGTGTGGAGTGGAGCCAGACACCTGAGGTCAAGTTTC 858  
Db 1096 ACCCTGAGGTCAATGCGTGTGTGGAGTGGAGCCAGACACCTGAGGTCAAGTTTC 1155  
QY 859 AACTGTGATGTGACGCGTGGAGGTGCATATGCCAAGAAAGCGCGGGAGGAGCAG 918  
Db 1156 AACTGTGATGTGACGCGTGGAGGTGCATATGCCAAGAAAGCGCGGGAGGAGCAG 1215  
QY 919 TACAACAGCAGCTACGCTGTGTGCTCAGCTCTCAGCTGCTGACACGAGCTGCGTGAAT 978  
Db 1216 TACAACAGCAGCTACGCTGTGTGCTCAGCTCTCAGCTGCTGACACGAGCTGCGTGAAT 1275  
QY 979 GGCAAGGAGTACAAGTGCAAGTCTCCAAAGAGCCCTCCAGCCGCCCATCGAGAAAC 1038  
Db 1276 GGCAAGGAGTACAAGTGCAAGTCTCCAAAGAGCCCTCCAGCCGCCCATCGAGAAAC 1335  
QY 1039 ATCTCAAAGCCAAAGGAGCGCCGAGAACCAAGGTGTACACCTGCCCCCATCCCG 1098  
Db 1336 ATCTCAAAGCCAAAGGAGCGCCGAGAACCAAGGTGTACACCTGCCCCCATCCCG 1395  
QY 1099 GATGAGCTGACCAAGAACCAAGGTGACGCTGCTGCTCAAGAGCTTCTATCCAGC 1158  
Db 1396 GATGAGCTGACCAAGAACCAAGGTGACGCTGCTGCTCAAGAGCTTCTATCCAGC 1455  
QY 1159 GATGAGCTGACCAAGAACCAAGGTGACGCTGCTGCTCAAGAGCTTCTATCCAGC 1218  
Db 1456 GATGAGCTGACCAAGAACCAAGGTGACGCTGCTGCTCAAGAGCTTCTATCCAGC 1515  
QY 1219 CCGTGTGAGCTCCGAGCGCT 1278  
Db 1516 CCGTGTGAGCTCCGAGCGCT 1575  
QY 1279 AGTGTGACGAGGAGGAGCT 1338  
Db 1576 AGTGTGACGAGGAGGAGCT 1635  
QY 1339 TACACGAGAGAGGAGCT 1377  
Db 1636 TACACGAGAGAGGAGCT 1674

RESULT 12  
ABQ74604

ID ABQ74604 standard; cDNA; 1674 BP.  
XX AC ABQ74604;  
XX DT 23-OCT-2002 (first entry)  
XX Mutation 1 Flt1(1-3 delta B)-Fc nucleotide sequence.  
DE DE Human; Flt1; vascular endothelial growth factor; VEGF; VEGF antagonist;  
XX KW psoriasis; wound healing; Flt1 receptor; antipsoriatic; antiinflammatory;  
XX KW vulnery; antiasthmatic; antirheumatic; antiarthritic; nephrotropic;  
XX KW ophthalmological; vascular permeability; oedema; inflammation; asthma;  
XX KW brain oedema; inflammatory disorder; rheumatoid arthritis; burn;  
XX KW kidney disease; eye disorder; age-related macular degeneration;  
XX KW diabetic retinopathy; gene; ss.  
XX OS Homo sapiens.  
OS Synthetic.  
XX Key Location/Qualifiers  
FH CDS 1..1674  
FT /\*tag= a  
FT /product= "Mut1:Flt1(1-3 delta B)-Fc protein"  
XX PN WO200260489-A1.  
XX PD 08-AUG-2002.  
XX PF 28-JAN-2002; 2002WO-US002466.  
XX PR 31-JAN-2001; 2001US-00773877.  
XX PA (REG-) REGENERON PHARM INC.  
XX PI Xia Y, Rudge JS, Yancopoulos GD;  
XX DR WPI; 2002-608488/65.  
XX DR P-PSDB; ABP52443.  
XX PT Treating psoriasis and enhancing wound healing in humans comprises the  
XX PT administration of a vascular endothelial cell growth factor (VEGF)  
XX PT antagonist.  
XX Example 11; Fig 13A-D; 179pp; English.  
XX The present invention describes a method for treating psoriasis and  
XX enhancing wound healing in a mammal or a human. The method comprises  
XX administering a vascular endothelial cell growth factor (VEGF) antagonist  
XX to the mammal or human. A VEGF antagonist has antipsoriatic,  
XX antiinflammatory, vulnery, antiasthmatic, antirheumatic, antiarthritic,  
XX nephrotropic and ophthalmological activities. The method can be used in  
XX treating psoriasis and enhancing wound healing in humans by administering  
XX VEGF antagonist. The method is also useful in treating clinical  
XX conditions characterised by vascular permeability, oedema or  
XX inflammation, such as brain oedema associated with injury, oedema  
XX associated with inflammatory disorders (e.g. rheumatoid arthritis),  
XX asthma, burns, kidney diseases, or eye disorders such as age-related  
XX macular degeneration and diabetic retinopathy. The method may also be  
XX used in making the polypeptide to decrease or inhibit plasma leakage and  
XX or vascular permeability. The present sequence encodes Mut1:Flt1(1-3  
XX delta B)-Fc which is used in an example from the present invention  
SQ Sequence 1674 BP; 495 A; 455 C; 378 G; 346 T; 0 U; 0 Other;  
Query Match 71.7%; Score 987.4; DB 6; Length 1674;  
Best Local Similarity 86.1%; Pred. No. 1.9e-229;  
Matches 1119; Conservative 0; Mismatches 171; Indels 9; Gaps 2;  
QY 79 AGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAATCCCGAAATTTATACATG 138  
Db 385 AGTGATACAGGTAGACCTTTCGTAGAGATGTACAGTGAATCCCGAAATTTATACATG 444  
QY 139 ACTGAAGGAGGAGCTGCTGCTATTCCTGCGGGTTACGTACCTAACATCACTGTTACT 198

445	Db	 ACTGAAGGAAGGAGCTCGTCA TTCCCTCGCGGGTTACGTACACCTAAACATCATCTGTTACT	504
199	Qy	TTAAAAAGTTTCCACTTGGACACTTTGATCCTCATGGAAGAACGCATAA TCTGGACAGT	258
505	Db	TTAAAAAGTTTCCACTTGGACACTTTGATCCTCATGGAAGAACGCATAA TCTGGACAGT	564
259	Qy	AGAAAGGGCTTCATCATATCAATGCAACGTACAAAGAAATAGGGCTTCTG ACCTGTGAA	318
565	Db	AGAAAGGGCTTCATCATATCAATGCAACGTACAAAGAAATAGGGCTTCTG ACCTGTGAA	624
319	Qy	GCAACAGTCAATGGGCATTTGTTAAGACAAA CTATCTCACATCGACAAA CCAATACA	378
625	Db	GCAACAGTCAATGGGCATTTGTTAAGACAAA CTATCTCACATCGACAAA CCAATACA	684
379	Qy	ATCATAGATGTGGTTCTTGAGTCCGTCTCATGTGAATTCGAATCTATCTG TTGGAGAAAGCTT	438
685	Db	ATCATAGATGTCCAAATTAAGACACACCCAGCCAGTCAAA TTACTTTAGAGGCCATACTCTTT	744
439	Qy	GTCTTAAATGTACAGCAAGAACTGAACTAAATGTGGGATTTGACTTTCAA CTGGGAATAC	498
745	Db	GTCTCTCAATGTACTGTCTACCACTCCCTTGAACACGAGAGTTCAA ATGA CTGGAGTTAC	804
499	Qy	CTTTCTTCGAAGCATACGACATAAGAAA CTTTGTAAACCGGACCTTAA AAAA CCCCAGTCTGGG	558
805	Db	CCTGATGAAATTTGACCAAGCAA TCCCATGTGCCAACATATCTTACAGTGTCTTACTATT	864
559	Qy	AGTCAGATGAAGAAATTTTGGAGCACCTTAACTATAGATGGTGTAA CCCCGGAGTGACCAA	618
865	Db	GACAAAATGCAAGACAAAGAACAAAGGACTTTTATCTTGTCTGTGTAA --- GGAGTGGACCA	921
619	Qy	GGATTGTACACCTGTGCAGCATCCAGTGGGTGTATGACCAAGAAAGACAG CATTTTGTCT	678
922	Db	TCATTTCAAATCTGTTAACACCTC-----AGTGCATATATATGATAAGCAGGCCCGGGC	975
679	Qy	AGGTCCTAATGAAAAGGACAA AAATCTCACATGCCCCACCGTGCC CAGCACCTGAACTCTCTG	738
976	Db	GAGCCCAAATCTTGTGACAA AACTCACATGCCCCACCGTGCC CAGCACCTGAACTCTCTG	1035
739	Qy	GGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCGAAGACACCC TCATGATCTCCCGG	798
1036	Db	GGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCGAAGACACCC TCATGATCTCCCGG	1095
799	Qy	ACCCTCAGGTGCACATGCTGGTGGAGCTGAGCCAGCAAGACACCT GAGGTCAAGTTC	858
1096	Db	ACCCTCAGGTGCACATGCTGGTGGTGGAGCTGAGCCACGAGACCT GAGGTCAAGTTC	1155
859	Qy	AACGTGTA CGTGGACGGCGTGGAGGTGCATAATGCCAAGACAA AGCCGCGGGAGGACGAG	918
1156	Db	AACGTGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAA AGCCGCGGGAGGACGAG	1215
919	Qy	TACAAACGACGTCACGTGTGGTCAGGTCCTTACCGTCTCTGCAC AGGACTGGCTGAAT	978
1216	Db	TACAAACGACGTCACGTGTGGTCAGGTCCTTACCGTCTCTGCAC AGGACTGGCTGAAT	1275
979	Qy	GGCAAGAGTACAGTGC CAAGTCTCCAA CAAAAGCCCTCC CAGCCCCCATCGAGAA AAC	1038
1276	Db	GGCAAGAGTACAGTGC CAAGTCTCCAA CAAAAGCCCTCC CAGCCCCCATCGAGAA AAC	1335
1039	Qy	ATCTCCAAAGCCAAAGGCGACCCCGAGAA CCA CAGGTGTACACCTTC GCCCATCC CCCG	1098
1336	Db	ATCTCCAAAGCCAAAGGCGACCCCGAGAA CCA CAGGTGTACACCTTC GCCCATCC CCCG	1395
1099	Qy	GATGAGCTGACCAAGAA ACGAGTTCAGCTTCGCTGAC CTGGTCA AAGGCTTCTATCC CAGC	1158
1396	Db	GATGAGCTGACCAAGAA ACGAGTTCAGCTTCGCTGAC CTGGTCA AAGGCTTCTATCC CAGC	1455
1159	Qy	GACATCCCGTGGAGTGGGAGAGCAATGGG CAGCCGAGACAA CTACAGACCA CGCCT	1218
1456	Db	GACATCCCGTGGAGTGGGAGAGCAATGGG CAGCCGAGAGCAATGGG CAGCCGAGACAA CTACAGACCA CGCCT	1515
1219	Qy	CCCGTGTGGA CTCCGACGGCTCCTCTTCTCTTACAGCAAGCTTCA CCGTGGACAGAGC	1278

Db	1516	CCCGTGTGACTCCGACGGCTCTCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGC	1578
Qy	1279	AGGTGGCAGCAGGGGAACGCTTTCTCATGCTCCGCTGATGCATCAGGCTCTGCACAACCCAC	1338
Db	1576	AGGTGGCAGCAGGGGAACGCTTTCTCATGCTCCGCTGATGCATCAGGCTCTGCACAACCCAC	1635
Qy	1339	TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA	1377
Db	1636	TACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA	1674
RESULT 13			
AAA91073			
ID	AAA91073 standard; DNA; 1704 BP.		
XX			
AC	AAA91073;		
XX			
DT	05-APR-2001 (first entry)		
XX			
DE	Flt1 receptor fusion protein Mut4:Flt1(1-3R-N)-Fc coding sequence.		
XX			
KW	Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic;		
KW	plasma leakage; vascular permeability; IGG Fc region; ss.		
XX			
OS	Unidentified.		
XX			
FH	Key Location/Qualifiers		
FT	CDS 1..1704		
FT	/*tag= a		
FT	/product= "Flt1(1-3R-N)-Fc"		
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PN	WO200075319-A1.		
XX			
PD	14-DEC-2000.		
XX			
PF	23-MAY-2000; 2000WO-US014142.		
XX			
PR	08-JUN-1999; 99US-0138133P.		
XX			
PA	(REGE-) REGENERON PHARM INC.		
XX			
PI	Papadopoulos NJ, Davis S, Yancopoulos GD;		
XX			
DR	WPI: 2001-071076/08.		
DR	P-PSDB; AAY97593.		
XX			
PT	Nucleic acid molecule encoding mammalian phospholipid transfer protein,		
PT	and its fragments, useful for diagnosis, evaluation, and treatment of		
PT	diseases associated with the gene expression and for producing model		
PT	systems.		
XX			
FS	Claim 9; Fig 16; 159pp; English.		
XX			
CC	This sequence encodes a fusion protein of the invention between the Flt1		
CC	receptor and the Fc region of IgG. The specification relates to modified		
CC	chimeric polypeptides with improved pharmacokinetics. The modified		
CC	chimeric polypeptides are preferably Flt1 receptor polypeptides that have		
CC	been modified to improve their pharmacokinetic profile. The polypeptides		
CC	can be used to decrease or inhibit plasma leakage and/or vascular		
CC	permeability in a mammal		
XX			
SQ	Sequence 1704 BP; 508 A; 461 C; 385 G; 350 T; 0 U; 0 Other;		
Query Match			
Best Local Similarity 71.3%; Score 982.4; DB 5; Length 1704;			
Matches 1132; Conservative 0; Mismatches 161; Indels 33; Gaps 2;			
Qy	79	AGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAATCCCGAAATTATACACATG	138
Db	385	AGTGATACAGGTAGACCTTTCGTAGAGATGTACAGTGAATCCCGAAATTATACACATG	444
Qy	139	ACTGAAGAAAGGAGGAGCTCGTCATTCCCTCGCGGGTTACGTCACCTAACATCACTGTTACT	198

Db 445 ACTGAGGAAGGAGCTCGTCAATTCCTCGCGGGTACGTCACCTAACATCACTGTACT 504  
Qy 199 TTAAGAAAGTTTCCACTTTCACACTTTGATCCCTGATGGAAGACGCATAATCTGGGACAGT 258  
Db 505 TTAAGAAAGTTTCCACTTTCACACTTTGATCCCTGATGGAAGACGCATAATCTGGGACAGT 564  
Qy 259 AGAAGGGCTTATCATATCAATAGCAACGTAACAAGAAATAGGGCTTTCGACTGTGAA 318  
Db 565 AGAAGGGCTTTCATCATATCAATAGCAACGTAACAAGAAATAGGGCTTTCGACTGTGAA 624  
Qy 319 GCAACAGTCAATGGGATTTGTATAGACAAATATCTACACATCGACAACCAATACA 378  
Db 625 GCAACAGTCAATGGGATTTGTATAGACAAATATCTACACATCGACAACCAATACA 694  
Qy 379 ATCATAGATGTGTTCTGAGTCCGCTCTCATGGAATTGAACATATCTGTGGAGAAAGCTT 438  
Db 685 ATCATAGATGTCCAAATAAGCAACACACGCCAGTCAAAATTAATTAGAGCCCATCTCTT 744  
Qy 439 GTCTTAAATTGTACAGCAAGAACTGAACATAAATGTGGGATTTGACTTCAACTGGGAATAC 498  
Db 745 GTCTCAATTTGTACTGTACCACTCCCTTGAACACGAGAGTTCAAAATGACCTGGAGTTAC 804  
Qy 499 CTTCTTCGAGCATGAGCATAGAAACTTGTAAACGAGACCTAAACCCAGTCTGGG 558  
Db 805 CTTGATGAAAGAAATAAGAACGCTTCGTAAGCGGACGAATTGACCAAGCAATTC--- 860  
Qy 559 AGTGAGATGAAGAAATTTTGGACACCTTAACATATAGATGGTGTAAACCCGAGTGACCAA 618  
Db 861 --CCATGCCACATATTTACAGTGTCTTACTATTGACAAATGAGAACAAAGACAAA 918  
Qy 619 GGATTTACACCTGTGAGCATCCAGTGGGCTGATGACCAAGAAAGAACAGCATTTGTC 678  
Db 919 GGACTTTATATCTGTGTGTAAGAGTGGACCATCATTCAAATCTGTTAACACCTCAGTG 978  
Qy 679 AGGGTCCATGAAA-----GGACAAACTCACATGC 711  
Db 979 CATATATATATAAGACAGCGCCCGGCGAGCCCAAAATCTTTGTGACAAAATCTACATGC 1038  
Qy 712 CCACCGTGCCGACACCTGAATCTCTGGGGGACCGTCACTCTCTCTTCCCGCCCAAAA 771  
Db 1039 CCACCGTGCCGACACCTGNACTCTTGGGGGACCGTCACTCTCTCTTCCCGCCCAAAA 1098  
Qy 772 CCAAGGACACCTCATATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTG 831  
Db 1099 CCAAGGACACCTCATATCTCTCCGACCCCTGAGTCACTGCTGCTGGTGGTGGACGTG 1158  
Qy 832 AGCCAGAGACCTGAGTCAAGTTCAACTGTGTAGTGAACCGCGTGGAGGTGCATAT 891  
Db 1159 AGCCAGAGACCTGAGTCAAGTTCAACTGTGTAGTGAACCGCGTGGAGGTGCATAT 1218  
Qy 892 GCCAAGACAAAGCCGGGAGGAGCAGTACAACAGCAGCTACCGTGTGGTCAAGCGTCTC 951  
Db 1219 GCCAAGACAAAGCCGGGAGGAGCAGTACAACAGCAGCTACCGTGTGGTCAAGCGTCTC 1278  
Qy 952 ACCGTCTGTGACAGGACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTCTTCAACAAA 1011  
Db 1279 ACCGTCTGTGACAGGACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTCTTCAACAAA 1338  
Qy 1012 GCCCTCCAGCCCGCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGAACCA 1071  
Db 1339 GCCCTCCAGCCCGCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGAACCA 1398  
Qy 1072 CAGGTGTACACCTGTGCCCCCATCCCGGATGAGTGAACCAAGAACACAGGTGACCGTGACC 1131  
Db 1399 CAGGTGTACACCTGTGCCCCCATCCCGGATGAGTGAACCAAGAACACAGGTGACCGTGACC 1458  
Qy 1132 TGCCTGGTCAAAGGCTTCTATCCAGCGCATCCCGTGGAGTGGGAGAGCAATGGGCGAG 1191  
Db 1459 TGCCTGGTCAAAGGCTTCTATCCAGCGCATCCCGTGGAGTGGGAGAGCAATGGGCGAG 1518  
Qy 1192 CCGGAGAACAACTACAAGACCAAGCTCCGTGCTGAGTCCGACGGCTCTTCTTCTCCTC 1251  
Db 1519 CCGGAGAACAACTACAAGACCAAGCTCCGTGCTGAGTCCGACGGCTCTTCTTCTCCTC 1578

Qy 1252 TACAGCAAGCTCACCGTGGACAAAGAGCAGGTGCGACAGGGGAACGTTCTTCATGCTCC 1311  
Db 1579 TACAGCAAGCTCACCGTGGACAAAGAGCAGGTGCGACAGGGGAACGTTCTTCATGCTCC 1638  
Qy 1312 GTGATGCATGAGGCTCTGCACAAACCACTACACGCAAGAGCCTTCCCTGTCTCCGGGT 1371  
Db 1639 GTGATGCATGAGGCTCTGCACAAACCACTACACGCAAGAGCCTTCCCTGTCTCCGGGT 1698  
Qy 1372 AAATGA 1377  
Db 1699 AAATGA 1704  
RESULT 14  
ABQ74607  
ID ABQ74607 standard; cDNA; 1704 BP.  
XX  
AC ABQ74607;  
XX  
DT 23-OCT-2002 (first entry)  
XX  
DE Mutation 4 Flt1(2-3 R->N)-Fc nucleotide sequence.  
XX  
KW Human; Flt1; vascular endothelial growth factor; VEGF; VEGF antagonist;  
KW psoriasis; wound healing; Flt1 receptor; antipsoriatic; antiinflammatory;  
KW vulnery; antiasthmatic; antirheumatic; antiarthritic; nephrotropic;  
KW ophthalmological; vascular permeability; oedema; inflammation; asthma;  
KW brain oedema; inflammatory disorder; rheumatoid arthritis; burn;  
KW kidney disease; eye disorder; age-related macular degeneration;  
KW diabetic retinopathy; gene; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key  
FT CDS 1..1704  
FT /tag= a  
FT /product= "Mut4:Flt1(2-3 R->N)-Fc protein"  
XX  
PN WO200260489-A1.  
XX  
PD 08-AUG-2002.  
XX  
PF 28-JAN-2002; 2002WO-US002466.  
XX  
PR 31-JAN-2001; 2001US-00773877.  
XX  
PA (REG-) REGENERON PHARM INC.  
XX  
PI Xia Y, Rudge JS, Yancopoulos GD;  
XX  
XX WPI; 2002-508488/65.  
DR P-PSDB; ABP52446.  
XX  
PT Treating psoriasis and enhancing wound healing in humans comprises the  
PT administration of a vascular endothelial cell growth factor (VEGF)  
PT antagonist.  
XX  
PS Example 14; Fig 16A-D; 179pp; English.  
XX  
CC The present invention describes a method for treating psoriasis and  
CC enhancing wound healing in a mammal or a human. The method comprises  
CC administering a vascular endothelial cell growth factor (VEGF) antagonist  
CC to the mammal or human. A VEGF antagonist has antipsoriatic,  
CC antiinflammatory, vulnery, antiasthmatic, antirheumatic, antiarthritic,  
CC nephrotropic and ophthalmological activities. The method can be used in  
CC treating psoriasis and enhancing wound healing in humans by administering  
CC VEGF antagonist. The method is also useful in treating clinical  
CC conditions characterised by vascular permeability, oedema or  
CC inflammation, such as brain oedema associated with injury, oedema  
CC associated with inflammatory disorders (e.g. rheumatoid arthritis),  
CC asthma, burns, kidney diseases, or eye disorders such as age-related

CC	macular degeneration and diabetic retinopathy. The method may also be		
CC	used in making the polypeptide to decrease or inhibit plasma leakage and		
CC	or vascular permeability. The present sequence encodes Mut4:Flt1(2-3 R-		
CC	>N)-Fc which is used in an example from the present invention		
XX			
SQ	Sequence 1704 BP; 508 A; 461 C; 385 G; 350 T; 0 U; 0 Other;		
	Query Match 71.3%; Score 982.4; DB 6; Length 1704;		
	Best Local Similarity 85.4%; Pred. No. 3.2e-228;		
	Matches 1132; Conservative 0; Mismatches 161; Indels 33; Gaps 2;		
QY	79 AGTGATACCGGTAGACCTTTCGTGAGATGATACAGTGAATCCCGGAAATTTATACATG 138	Db	1279 ACCGTCTCTGCACAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAGGCTCTCCACAAA 1338
Db	385 AGTGATACAGGTAGACCTTTCGTGAGATGATACAGTGAATCCCGGAAATTTATACATG 444	QY	1012 GCCCTCCAGCCCCCATATCGAGAAAAACCATCTTCCAAGCCAAAGGGCAGCCCCGAGAACCA 1071
QY	139 ACTGAAGGAAGGAGCTCGTCAATTCCTCCCGGGTTACGTCACCTAACATCATCTGTACT 198	Db	1339 GCCCTCCAGCCCCCATATCGAGAAAAACCATCTTCCAAGCCAAAGGGCAGCCCCGAGAACCA 1398
Db	445 ACTGAAGGAAGGAGCTCGTCAATTCCTCCCGGGTTACGTCACCTAACATCATCTGTACT 504	QY	1072 CAGGTGTACACCTGCCCCCATCCCGGATGAGCTGACCAAGAACCCAGGTCAAGCTGACC 1131
QY	199 TTAATAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAACCGCATATCTGGGACAGT 258	Db	1399 CAGGTGTACACCTGCCCCCATCCCGGATGAGCTGACCAAGAACCCAGGTCAAGCTGACC 1458
Db	505 TTAATAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAACCGCATATCTGGGACAGT 564	QY	1132 TGCTTGGTCAAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG 1191
QY	259 AGAAAGGGCTTCATCATATCAAAATGCAACGTACAAAGAAATAGGGCTTCTGACCTGTGAA 318	Db	1459 TGCTTGGTCAAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGCAATGGGCAG 1518
Db	565 AGAAAGGGCTTCATCATATCAAAATGCAACGTACAAAGAAATAGGGCTTCTGACCTGTGAA 624	QY	1192 CCGGAGAACCAACTACAAGACACCGCTCCCGTGTGGACTCCGACGGCTCTCTTCTTCTCCTC 1251
QY	319 GCAACAGTCAATGGGCATTTGTATAGACAAACTATCTCACATACGACAAACCAATACA 378	Db	1519 CCGGAGAACCAACTACAAGACACCGCTCCCGTGTGGACTCCGACGGCTCTCTTCTTCTCCTC 1578
Db	625 GCAACAGTCAATGGGCATTTGTATAGACAAACTATCTCACATACGACAAACCAATACA 684	QY	1252 TACAGCAAGCTCACCGTGGACAAAGACGAGGTGGCAGCAGGGGAACGCTTCTCATGCTCC 1311
QY	379 ATCATAGATGTGGTCTGAGTCGGTCTCATGGAATTTGAATCTATCTGTTGGAGAAAGCTT 438	Db	1579 TACAGCAAGCTCACCGTGGACAAAGACGAGGTGGCAGCAGGGGAACGCTTCTCATGCTCC 1638
Db	685 ATCATAGATGTCCAAATAAGCACACACGCCAGTCAAAATTAATTAGAGGCCATCTCTT 744	QY	1312 GTGATGCATGAGGCTCTGCACAAACCACTACACGACAGAGGCTCTCCCTGTCTCCGGGT 1371
QY	439 GTCTTAAATTTGTACAGCAAGAACTGAATGTTGGGATTTGACTTCAACTGGGAATAC 498	Db	1639 GTGATGCATGAGGCTCTGCACAAACCACTACACGACAGAGGCTCTCCCTGTCTCCGGGT 1698
Db	745 GTCTCAATTTGACTGCTACCACTCCCTTGAACACGAGAGTTCAATGACCTGGAGTTAC 804		
QY	499 CTTCTTCCGAAGCATCAGCATAGAAACTTTGTTAAACCGAGACCTAAAAACCCAGTCTGG 558		
Db	805 CTTGATGAAAAAATAAGAACGCTTCCGTGAAGGCGACGAATTGACCAAGCAATTC--- 860		
QY	559 AGTGAGATGAAGAAATTTTGACCACTTAACTATAGATGGTGTAAACCGGAGTACCAA 618		
Db	861 --CCATGCCAACATATTTCTACAGTGTCTTACTATTGACAAAATGCGAACAAGACAAA 918		
QY	619 GGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAGAAAGAACAGCACATTTGTC 678		
Db	919 GGACTTTATCTGTCTGTTAGGAGTGGACCATCATTTCAAATCTGTTTAAACACCTCAGTG 978		
QY	679 AGGGTCCATGAAA-----GGACAAAATCTCACATGC 711		
Db	979 CATATATATGATAAAGCAGCGCCGGGAGCCCAAAATCTTGTGACAAAATCTCACATGC 1038		
QY	712 CCACCGTGCCAGCACCTGAACTCTGGGGGAGCCGTCACTTCTCTTCCCCCAAAA 771		
Db	1039 CCACCGTGCCAGCACCTGAACTCTGGGGGAGCCGTCACTTCTCTTCCCCCAAAA 1098		
QY	772 CCCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTCAATGCGTGGTGGAGCGTG 831		
Db	1099 CCCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTCAATGCGTGGTGGAGCGTG 1158		
QY	832 AGCCAGAAAGACCTGAGTCAAGTTCACTGTTAGTGGAGCGGGTGGAGGTGCATAAT 891		
Db	1159 AGCCAGAAAGACCTGAGTCAAGTTCACTGTTAGTGGAGCGGGTGGAGGTGCATAAT 1218		
QY	892 GCCAAGACAAAGCCGGGAGGAGAGTACAAACAGCACGTTACGTTGGTGGTGGTGGTGGT 951		
Db	1219 GCCAAGACAAAGCCGGGAGGAGAGTACAAACAGCACGTTACGTTGGTGGTGGTGGTGGT 1278		
QY	952 ACCGTCTCTGCACGAGCTGGCTGAATGGCAAGGAGTACAAGTGCAGGCTCTCCACAAA 1011		

Db	1279	ACCGTCTCTGCACAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAGGCTCTCCACAAA	1338
QY	1012	GCCCTCCAGCCCCCATATCGAGAAAAACCATCTTCCAAGCCAAAGGGCAGCCCCGAGAACCA	1071
Db	1339	GCCCTCCAGCCCCCATATCGAGAAAAACCATCTTCCAAGCCAAAGGGCAGCCCCGAGAACCA	1398
QY	1072	CAGGTGTACACCTGCCCCCATCCCGGATGAGCTGACCAAGAACCCAGGTCAAGCTGACC	1131
Db	1399	CAGGTGTACACCTGCCCCCATCCCGGATGAGCTGACCAAGAACCCAGGTCAAGCTGACC	1458
QY	1132	TGCTTGGTCAAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG	1191
Db	1459	TGCTTGGTCAAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGCAATGGGCAG	1518
QY	1192	CCGGAGAACCAACTACAAGACACCGCTCCCGTGTGGACTCCGACGGCTCTCTTCTTCTCCTC	1251
Db	1519	CCGGAGAACCAACTACAAGACACCGCTCCCGTGTGGACTCCGACGGCTCTCTTCTTCTCCTC	1578
QY	1252	TACAGCAAGCTCACCGTGGACAAAGACGAGGTGGCAGCAGGGGAACGCTTCTCATGCTCC	1311
Db	1579	TACAGCAAGCTCACCGTGGACAAAGACGAGGTGGCAGCAGGGGAACGCTTCTCATGCTCC	1638
QY	1312	GTGATGCATGAGGCTCTGCACAAACCACTACACGACAGAGGCTCTCCCTGTCTCCGGGT	1371
Db	1639	GTGATGCATGAGGCTCTGCACAAACCACTACACGACAGAGGCTCTCCCTGTCTCCGGGT	1698
QY	1372	AAATGA	1377
Db	1699	AAATGA	1704
RESULT 15			
AAA91077			
ID	AAA91077 standard; DNA; 1704 BP.		
XX	AAA91077;		
XX	AC		
XX	05-APR-2001 (first entry)		
DT	05-APR-2001 (first entry)		
XX	Flt1 receptor protein Flt1(1-3)-Fc coding sequence.		
DE	Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic;		
XX	Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic;		
KW	plasma leakage; vascular permeability; IgG Fc region; ss.		
KW	Unidentified.		
OS	Key		
XX	Location/Qualifiers		
FH	1. .1704		
FT	/*tag= a		
FT	/product= "Flt1(1-3)-Fc"		
XX	WO200075319-A1.		
PN	14-DEC-2000.		
XX	23-MAY-2000; 2000WO-US014142.		
XX	08-JUN-1999; 99US-0138133P.		
XX	(REG- ) REGENERON PHARM INC.		
PA	Papadopoulos NJ, Davis S, Yancopoulos GD;		
XX	WPI; 2001-071076/08.		
DR	P-PSDB; AAY97597.		
XX	Nucleic acid molecule encoding mammalian phospholipid transfer protein,		
PT	and its fragments, useful for diagnosis, evaluation, and treatment of		
PT	diseases associated with the gene expression and for producing model		
PT	systems.		
XX	Example 11; Fig 10; 159pp; English.		
PS			
XX			

CC This sequence encodes a fusion protein of the invention between the Flt1  
CC receptor and the Fc region of IgG. The specification relates to modified  
CC chimeric polypeptides with improved pharmacokinetics. The modified  
CC chimeric polypeptides are preferably Flt1 receptor polypeptides that have  
CC been modified to improve their pharmacokinetic profile. The polypeptides  
CC can be used to decrease or inhibit plasma leakage and/or vascular  
CC permeability in a mammal

XX

SQ Sequence 1704 BP; 508 A; 460 C; 386 G; 350 T; 0 U; 0 Other;

Query Match 71.2%; Score 980.8; DB 5; Length 1704;  
Best Local Similarity 85.3%; Pred. No. 7.8e-228;  
Matches 1131; Conservative 0; Mismatches 162; Indels 33; Gaps 2;

QY	79	AGTGATACCGGTAGACCTTTCTGATAGATGATACAGTGAATCCCGAAATATATACATG	138
DB	385	AGTGATACAGGTAGACCTTTCTGATAGATGATACAGTGAATCCCGAAATATATACATG	444
QY	139	ACTGAAGGAAGGAGCTCGTCAATTCCTCGCGGTTCAGTCACTTAACATCACTGTTACT	198
DB	445	ACTGAAGGAAGGAGCTCGTCAATTCCTCGCGGTTCAGTCACTTAACATCACTGTTACT	504
QY	199	TTAATAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAACGCATAATCTGGACAGT	258
DB	505	TTAATAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAACGCATAATCTGGACAGT	564
QY	259	AGAAAGGGCTTCATCATATCAATGCAACGTACAAAGAAATAGGGCTTCGACCTGTGAA	318
DB	565	AGAAAGGGCTTCATCATATCAATGCAACGTACAAAGAAATAGGGCTTCGACCTGTGAA	624
QY	319	GCAACAGTCAATGGCAATTTGTATAGACAAATCTCTACATCGACAAACCAATACA	378
DB	625	GCAACAGTCAATGGCAATTTGTATAGACAAATCTCTACATCGACAAACCAATACA	684
QY	379	ATCATAGATGGTTCGTAGTCCGTCTCATGGATTGAATCTGTGGAGAAAGCTT	438
DB	685	ATCATAGATGCCAAATTAAGACACACACGCCAGTCAAAATTAATTAGAGGCCATCTCTT	744
QY	439	GTCTTAAATTTGTACAGCAAGAACTGAATTAATGTGGGATTCGACTTCAACTCGGAATAC	498
DB	745	GTCTTAAATTTGTACAGCAAGAACTGAATTAATGTGGGATTCGACTTCAACTCGGAATAC	804
QY	499	CTTTCTTCGAAGCATCAGCAATAGAACTTTGTAAACCGAGACCTAAACCCAGTCTGGG	558
DB	805	CCT-----CATGAAAAAATAAGAGAGCTTCCGTAAGGCGACGAATTTGACCAAGCAAT	858
QY	559	AGTGAGATGAAGAAATTTTGGACACCTTAACATATAGATGGTGTAAACCCGGAGTACAA	618
DB	859	TCCCATGCCAACATAATTCTACAGTGTCTTACTATTGACAAAAATGCAGAACAAAGACAA	918
QY	619	GGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAGAAAGAACAGCATTTGTC	678
DB	919	GGACTTTTACTTGTGTGTGAAGAGTGGACCATCATTCAAATCTGTTAAACCTCAGTG	978
QY	679	AGGGTCCATGAAAA-----GGACAAAACTCACATGC	711
DB	979	CATATATATGATAAAGCAGGCCCGGGGAGCCCAAAATCTTGTGACAAAACTCACATGC	1038
QY	712	CCACCGTCCCGAGCACTGAACTCTCGGGGGAGCCGTCACTCTTCTTCCCGCCCAAAA	771
DB	1039	CCACCGTCCCGAGCACTGAACTCTCGGGGGAGCCGTCACTCTTCTTCCCGCCCAAAA	1098
QY	772	CCCAAGGACACCTCATGATCTCCCGGACCCCTGAGTGCATGTCGTTGGTGGACGTG	831
DB	1099	CCCAAGGACACCTCATGATCTCCCGGACCCCTGAGTGCATGTCGTTGGTGGACGTG	1158
QY	832	AGCCACGAAGACCTCAGGTCAAGTTCACTGGTACGTGGACCGCGTGGAGGTGCATAAT	891
DB	1159	AGCCACGAAGACCTCAGGTCAAGTTCACTGGTACGTGGACCGCGTGGAGGTGCATAAT	1218
QY	892	GCCAAGCAAAAGCCGGGAGGAGAGTACAACAGCAAGTACCGTGTGTGTCAGCGTCTC	951
DB	1219	GCCAAGCAAAAGCCGGGAGGAGAGTACAACAGCAAGTACCGTGTGTGTCAGCGTCTC	1278

Search completed: September 23, 2005, 14:00:38  
Job time : 771 secs

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OM nucleic - nucleic search, using sw model

Run on: September 23, 2005, 13:12:56 ; Search time 4299 Seconds  
(without alignments)

12192.254 Million cell updates/sec

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Perfect score: 1377

Sequence: 1 atggtcagctactgggacac.....ccctgtctcggtaaatga 1377

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 68479088

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_hic:\*

4: gb\_est3:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_gss1:\*

9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	684	49.7	871	4 BG753979	BG753979 602709506
2	684	49.7	983	5 BQ708975	BQ708975 AGENCOURT
3	683	49.6	941	5 BQ712021	BQ712021 AGENCOURT
4	682.4	49.6	843	4 BM007897	BM007897 603617582
5	682.4	49.6	925	5 BQ709152	BQ709152 AGENCOURT
6	682.4	49.6	1022	3 CR611254	CR611254 full-leng
7	682.4	49.6	1048	3 CR595172	CR595172 full-leng
8	682.4	49.6	1090	3 CR612308	CR612308 full-leng
9	682.4	49.6	1091	3 CR604961	CR604961 full-leng
10	682.4	49.6	1093	3 CR616804	CR616804 full-leng
11	682.4	49.6	1098	3 CR626477	CR626477 full-leng
12	682.4	49.6	1100	3 CR612813	CR612813 full-leng
13	682.4	49.6	1102	3 CR601777	CR601777 full-leng
14	682.4	49.6	1102	3 CR625051	CR625051 full-leng
15	682.4	49.6	1103	3 CR595194	CR595194 full-leng
16	682.4	49.6	1104	3 CR591904	CR591904 full-leng
17	682.4	49.6	1106	3 CR613460	CR613460 full-leng
18	682.4	49.6	1106	3 CR620071	CR620071 full-leng
19	682.4	49.6	1107	3 CR598548	CR598548 full-leng
20	682.4	49.6	1109	3 CR614200	CR614200 full-leng
21	682.4	49.6	1109	3 CR619687	CR619687 full-leng
22	682.4	49.6	1111	3 CR606782	CR606782 full-leng
23	682.4	49.6	1114	3 CR593349	CR593349 full-leng
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26	682.4	49.6	1120	3 CR619868	CR619868 full-leng
27	682.4	49.6	1124	3 CR611468	CR611468 full-leng
28	682.4	49.6	1136	3 CR598462	CR598462 full-leng
29	682.4	49.6	1142	3 CR598316	CR598316 full-leng
30	682.4	49.6	1179	3 CR607277	CR607277 full-leng
31	682.4	49.6	1287	3 CR611016	CR611016 full-leng
32	682.4	49.6	1289	3 CR594000	CR594000 full-leng
33	681.4	49.5	851	5 BX346946	BX346946 BX346946
34	681.4	49.5	973	5 BQ706204	BQ706204 AGENCOURT
35	680.8	49.4	919	5 BQ709339	BQ709339 AGENCOURT
36	679.2	49.3	947	5 BQ709771	BQ709771 AGENCOURT
c	677	49.2	1013	5 BX360518	BX360518 AGENCOURT
38	676.8	49.2	897	5 BQ709144	BQ709144 AGENCOURT
39	676.6	49.1	757	4 BG674795	BG674795 602620925
40	676.6	49.1	914	5 BQ712363	BQ712363 AGENCOURT
41	676	49.1	881	5 BQ711291	BQ711291 AGENCOURT
42	672	48.8	892	4 BG397723	BG397723 602438784
43	672	48.8	897	4 BM008412	BM008412 603617406
c	671.8	48.8	1015	5 BX367600	BX367600 BX367600
45	671.4	48.8	856	5 BQ709859	BQ709859 AGENCOURT

#### ALIGNMENTS

RESULT 1  
BG753979 871 bp mRNA linear EST 15-MAY-2001  
LOCUS 602709506F1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4846201 5',  
DEFINITION mRNA sequence.

ACCESSION BG753979 GI:14064632

VERSION EST.

KEYWORDS Homo sapiens (human)

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

NIH-MGC http://mgs.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

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Email: cgapbs-x@mail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.W.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLC1686 row: k column: 02

High quality sequence stop: 848.

Location/Qualifiers

1..871

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:4846201"

/tissue\_type="primary B-cells from tonsils (cell line)"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH MGC 48"

/note="Organ: B-cells; Vector: pOTB7; Site: 1: XhoI;

Site 2: EcoRI; cDNA made by oligo-dT priming.

Directionally cloned into EcoRI/XhoI sites using the

following 5' adaptor: GGCACGAG(G). Size-selected >500bp

for average insert size 1.8kb. Library constructed by Ling

Hong in the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH\_MGC Library.

ORIGIN

Query Match 49.7%; Score 684; DB 4; Length 871;  
Best Local Similarity 100.0%; Pred. No. 4.7e-179; Indels 0; Gaps 0;  
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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754 TTCTCTTCCCTCCCAAAACCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTACA 813  
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97 TTCTCTTCCCTCCCAAAACCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTACA 156  
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814 TGGTGTGTGTGACGTGACGACAGCACCCTGAGTCAAGTTCACCTGATGTCGTCGAC 873  
|||||  
157 TGGTGTGTGTGACGTGACGACAGCACCCTGAGTCAAGTTCACCTGATGTCGTCGAC 216  
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874 GCGTGTGAGGTGATATGTCACAGACAAAGCCCGGGAGGAGCAGTACAAACAGCAGTAC 933  
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217 GCGTGTGAGGTGATATGTCACAGACAAAGCCCGGGAGGAGCAGTACAAACAGCAGTAC 276  
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934 CGTGTGTGAGGTCTCTCAGCTCCCGTTCGACAGGACCTGGCTGAATGGCAAGGATCAAG 993  
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277 CGTGTGTGAGGTCTCTCAGCTCCCGTTCGACAGGACCTGGCTGAATGGCAAGGATCAAG 336  
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994 TGCAAGGTCTCCAAAGAGCCCTCCAGCCGCCCATCGAGAAACCATCTCCAAAGCCAA 1053  
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337 TGCAAGGTCTCCAAAGAGCCCTCCAGCCGCCCATCGAGAAACCATCTCCAAAGCCAA 396  
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1054 GGGCAGCCCGGAGAACACAGGTGTACACCTGCTCCGCCCATCCCGGGATGAGCTGACCAAG 1113  
|||||  
397 GGGCAGCCCGGAGAACACAGGTGTACACCTGCTCCGCCCATCCCGGGATGAGCTGACCAAG 456  
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1114 AACAGGTGAGCTGACCTGCTGCTGTCAGAGGCTTCTATCCAGCAGCATCGCCGTGGAG 1173  
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457 AACAGGTGAGCTGACCTGCTGCTGTCAGAGGCTTCTATCCAGCAGCATCGCCGTGGAG 516  
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1174 TGGGAGAGCAATGGGACGCGAGAACCACTACAAGACACGCTCCCGTGTGGACTCC 1233  
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1234 GACGGTCTCTTCTCTACAGCAAGCTCACCGTGGACAAAGAGCAGGTGGCAGCAGGGG 1293  
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1294 AACGTCTTCTCATGCTCCGTCATGATGATGAGGCTTGCACCAACCTACAGCAGAGAGC 1353  
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637 AACGTCTTCTCATGCTCCGTCATGATGAGGCTTGCACCAACCTACAGCAGAGAGC 696  
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1354 CTCTCCCTGTCTCCGGTAAATGA 1377  
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RESULT 2  
LOCUS B0708975  
DEFINITION AGENCOURT\_8353514 NIH\_MGC\_113 Homo sapiens cDNA clone IMAGE:6279683  
5', mRNA sequence.  
ACCESSION B0708975  
VERSION B0708975.1 GI:21847874  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 983)  
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-i@mail.nih.gov](mailto:cgapbs-i@mail.nih.gov)  
Tissue Procurement: Dr. Mark Watson  
cDNA Library Preparation: Rubin Laboratory

cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLCM2469 row: k column: 12  
High quality sequence stop: 604.  
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source Location/Qualifiers  
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/organism="Homo sapiens"  
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/clone="IMAGE:6279683"  
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/clone\_lib="NIH\_MGC\_113"  
/notes="Organ: spleen; Vector: pOTB7; Site: 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GGCAGAG(G) Library constructed by Ling Hong in the  
laboratory of Gerald M. Rubin (University of California,  
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and  
Superscript II RT (Life Technologies). Note: this is a  
NIH\_MGC Library."

## ORIGIN

Query Match 49.7%; Score 684; DB 5; Length 983;  
Best Local Similarity 100.0%; Pred. No. 4.9e-179; Indels 0; Gaps 0;  
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||  
24 GACAAACTCACATGCTCCACCGTGCACAGCACCCTCATGATCTCCCGGACCCCTGAGTC 83  
|||||

754 TTCTCTTCCCTCCCAAAACCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTACA 813  
|||||  
84 TTCTCTTCCCTCCCAAAACCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTACA 143  
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814 TGGTGTGTGTGACGTGACGACAGCACCCTGAGTCAAGTTCACCTGAGTGGAGTCAC 873  
|||||  
144 TGGTGTGTGTGACGTGACGACAGCACCCTGAGTCAAGTTCACCTGAGTGGAGTCAC 203  
|||||

874 GCGTGTGAGGTGATATGTCACAGACAAAGCCCGGGAGGAGCAGTACAAACAGCAGTAC 933  
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204 GCGTGTGAGGTGATATGTCACAGACAAAGCCCGGGAGGAGCAGTACAAACAGCAGTAC 263  
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934 CGTGTGTGAGGTCTCTCAGCTCCCGTTCGACAGGACCTGGCTGAATGGCAAGGATCAAG 993  
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264 CGTGTGTGAGGTCTCTCAGCTCCCGTTCGACAGGACCTGGCTGAATGGCAAGGATCAAG 323  
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994 TGCAGGTCTCCAAAGAGCCCTCCAGCCGCCCATCGAGAAACCATCTCCAAAGCCAA 1053  
|||||  
324 TGCAGGTCTCCAAAGAGCCCTCCAGCCGCCCATCGAGAAACCATCTCCAAAGCCAA 383  
|||||

1054 GGGCAGCCCGGAGAACACAGGTGTACACCTGCTCCGCCCATCCCGGGATGAGCTGACCAAG 1113  
|||||  
384 GGGCAGCCCGGAGAACACAGGTGTACACCTGCTCCGCCCATCCCGGGATGAGCTGACCAAG 443  
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1114 AACAGGTGAGCTGACCTGCTGCTGTCAGAGGCTTCTATCCAGCAGCATCGCCGTGGAG 1173  
|||||  
444 AACAGGTGAGCTGACCTGCTGCTGTCAGAGGCTTCTATCCAGCAGCATCGCCGTGGAG 503  
|||||

1174 TGGGAGAGCAATGGGACGCGGAGAACCACTACAAGACACGCTCCCGTGTGGACTCC 1233  
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504 TGGGAGAGCAATGGGACGCGGAGAACCACTACAAGACACGCTCCCGTGTGGACTCC 563  
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1234 GACGGTCTCTTCTCTACAGCAAGCTCACCGTGGACAAAGAGCAGGTGGCAGCAGGGG 1293  
|||||  
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1294 AACGTCTTCTCATGCTCCGTCATGATGAGGCTTGCACCAACCTACAGCAGAGAGC 1353  
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624 AACGTCTTCTCATGCTCCGTCATGATGAGGCTTGCACCAACCTACAGCAGAGAGC 683  
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[illegible]

## ORIGIN

Query Match 49.6%; Score 682.4; DB 4; Length 843;  
Best Local Similarity 99.9%; Pred. No. 1.3e-178;  
Matches 683; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 108 GACAAAACTCACATGCCACCGTCCCGAGCACCTCATGATCTCCCGGACCCCTGAGGTACACA 167  
QY 754 TTCTCTTTCCCCCAAAACCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTACACA 813  
DB 168 TTCTCTTTCCCCCAAAACCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTACACA 227  
QY 814 TGGGTGGTGGTGGAGCGGACCGGACCGGACCGGACCGGACCGGACCGGACCGGACCGGAC 873  
DB 228 TGGGTGGTGGTGGAGCGGACCGGACCGGACCGGACCGGACCGGACCGGACCGGACCGGAC 287  
QY 874 GGGGTGGAGTGCATATGTCACAGACAAAGCCGCGGAGGAGCAGTACACAGCAGCTAC 933  
DB 288 GGGGTGGAGTGCATATGTCACAGACAAAGCCGCGGAGGAGCAGTACACAGCAGCTAC 347  
QY 934 CGTGTGGTTCAGCGTCTCTCACCGTCTGACAGGACCTGGCTGAATGGCAAGGAGTACAAG 993  
DB 348 CGTGTGGTTCAGCGTCTCTCACCGTCTGACAGGACCTGGCTGAATGGCAAGGAGTACAAG 407  
QY 994 TGCAGGTCTTCCAAAGACCCCTCCAGCCCGGACCCCTGAGAAACCACTCTCCAAAGCCAAA 1053  
DB 408 TGCAGGTCTTCCAAAGACCCCTCCAGCCCGGACCCCTGAGAAACCACTCTCCAAAGCCAAA 467  
QY 1054 GGGCAGCCCGGAGAACCAAGGTGTACACCTGCGCCCGGACCCCTGAGAAACCACTCTCCAAAG 1113  
DB 468 GGGCAGCCCGGAGAACCAAGGTGTACACCTGCGCCCGGACCCCTGAGAAACCACTCTCCAAAG 527  
QY 1114 AACGAGGTTCAGCGTCTCTCTTCCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1173  
DB 528 AACGAGGTTCAGCGTCTCTCTTCCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 587  
QY 1174 TGGGAGAGCAATGGGAGCGGAGAACCACTAAGACCAAGCAGTACACAGCAGCTAC 1233  
DB 588 TGGGAGAGCAATGGGAGCGGAGAACCACTAAGACCAAGCAGTACACAGCAGCTAC 647  
QY 1234 GACGGTCTCTTCTCTCTTCT 1293  
DB 648 GACGGTCTCTTCTCTCTTCT 707  
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DB 768 CT 791

## RESULT 5

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LOCUS BQ709152 925 bp mRNA linear EST 16-JUL-2002  
DEFINITION AGENCOURT\_8485151 NIH\_MGC\_113 Homo sapiens cDNA clone IMAGE:6301245  
5', mRNA sequence.  
ACCESSION BQ709152  
VERSION BQ709152.1 GI:21848051  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 925)  
NIH-MGC <http://mgs.nci.nih.gov/>.  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-r@mail.nih.gov

## Tissue Procurement: Dr. Mark Watson

cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:

<http://image.llnl.gov>

Plate: L1CM2516 row: m column: 22

High quality sequence stop: 739.

## FEATURES

## source

Location/Qualifiers

1..925

/organism="Homo sapiens"

/mol\_type="mRNA"

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/clone="IMAGE:6301245"

/lab\_host="DH10B (phage-resistant)"

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/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GGCAGCAG(G). Library constructed by Ling Hong in the  
laboratory of Gerald M. Rubin (University of California,  
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and  
Superscript II RT (Life Technologies). Note: this is a  
NIH\_MGC Library."

## ORIGIN

Query Match 49.6%; Score 682.4; DB 5; Length 925;  
Best Local Similarity 99.9%; Pred. No. 1.3e-178;  
Matches 683; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 694 GACAAACTCACATGCCACCGTCCCGAGCACCTGAACTCTGGGGGACCGTCAGTC 753  
DB 48 GACAAAACTCACATGCCACCGTCCCGAGCACCTGAACTCTGGGGGACCGTCAGTC 107  
QY 754 TTCTCTTTCCCCCAAAACCCCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTACACA 813  
DB 108 TTCTCTTTCCCCCAAAACCCCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTACACA 167  
QY 814 TGGGTGGTGGTGGAGCGTGGAGCCACGAAGACCCCTGAGGTCAAAGTTCACCTGGTACGTGGAC 873  
DB 168 TGGGTGGTGGTGGAGCGTGGAGCCACGAAGACCCCTGAGGTCAAAGTTCACCTGGTACGTGGAC 227  
QY 874 GGGGTGGAGTGCATATGTCACAGACAAAGCCGCGGAGGAGCAGTACACAGCAGCTAC 933  
DB 228 GGGGTGGAGTGCATATGTCACAGACAAAGCCGCGGAGGAGCAGTACACAGCAGCTAC 287  
QY 934 CGTGTGGTTCAGCGTCTCTCTCACCGTCTGACAGGACCTGGCTGAATGGCAAGGAGTACAAG 993  
DB 288 CGTGTGGTTCAGCGTCTCTCTCACCGTCTGACAGGACCTGGCTGAATGGCAAGGAGTACAAG 347  
QY 994 TGCAGGTCTTCCAAAGACCCCTCCAGCCCGGACCCCTGAGAAACCACTCTCCAAAGCCAAA 1053  
DB 348 TGCAGGTCTTCCAAAGACCCCTCCAGCCCGGACCCCTGAGAAACCACTCTCCAAAGCCAAA 407  
QY 1054 GGGCAGCCCGGAGAACCAAGGTGTACACCTGCGCCCGGACCCCTGAGAAACCACTCTCCAAAG 1113  
DB 408 GGGCAGCCCGGAGAACCAAGGTGTACACCTGCGCCCGGACCCCTGAGAAACCACTCTCCAAAG 467  
QY 1114 AACGAGGTTCAGCGTCTCTCTTCCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1173  
DB 468 AACGAGGTTCAGCGTCTCTCTTCCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 527  
QY 1174 TGGGAGAGCAATGGGAGCGGAGAACCACTAAGACCAAGCAGTACACAGCAGCTAC 1233  
DB 528 TGGGAGAGCAATGGGAGCGGAGAACCACTAAGACCAAGCAGTACACAGCAGCTAC 587  
QY 1234 GACGGTCTCTTCTCTCTTCT 1293  
DB 588 GACGGTCTCTTCTCTCTTCT 647  
QY 1294 AACGTCCTTCT 1353

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Db      648 AACGCTCTTCATGCTCCGTCGATGATGAGGCTCTGCACAAACCACTACACACAGAGC 707
QY      1354 CTCTCCCTGTCTCCGGGTAATGA 1377
Db      708 CTCTCCCTGTCTCCGGGTAATGA 731

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DEFINITION
ACCESSION CR611254
VERSION   1
KEYWORDS  HTCC; CNSLT; cDNA.
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
          1 (bases 1 to 1022)
          Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
          Full-length cDNA libraries and normalization
          Unpublished
          Contact : Feng Liang Email : fliang@lifetech.com URL :
          http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
          Faraday Avenue
          2 (bases 1 to 1022)
          Genoscope.
          Direct Submission
          Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
          BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
          - Web : www.genoscope.cns.fr)
          1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
          end enriched, double-strand cDNA was digested with Not I and cloned
          into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
          was normalized. Library was constructed by Life Technologies, a
          division of Invitrogen.
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Best Local Similarity 99.9%; Pred. No. 1.4e-178;
Matches 683; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      694 GACAAACTCACATGCCACCGTCCGACGACCTGAACCTCTGGGGGACCGTCAGTC 753
Db      323 GACAAACTCACATGCCACCGTCCGACGACCTGAACCTCTGGGGGACCGTCAGTC 382
QY      754 TTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGACCCCTGAGGTCA 813
Db      383 TTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGACCCCTGAGGTCA 442
QY      814 TGGTGTGGTGGACGTGACGCCACGACGACCTCTGAGGTCAAGTTCAACTGTCGTGGAC 873
Db      443 TGGTGTGGTGGACGTGACGCCACGACGACCTCTGAGGTCAAGTTCAACTGTCGTGGAC 502
QY      874 GGGTGTGAGTGCATATGCAAGCAAAAGCCGGGAGAGAGAGATCAACACAGCGTAC 933
Db      503 GGGTGTGAGTGCATATGCAAGCAAAAGCCGGGAGAGAGAGATCAACACAGCGTAC 562
QY      934 CGTGTGTGAGGTCTTCACCGTCTTCGACGACGACCTGGCTGAATGSCAAGGAGTCAAG 993
Db      563 CGTGTGTGAGGTCTTCACCGTCTTCGACGACGACCTGGCTGAATGSCAAGGAGTCAAG 622
QY      994 TGCAAGGTCTTCAACAAAGCCCTCCACGACCCCATCGAGAAAACCATCTCTCAAAGCCAAA 1053

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Db      623 TGCAAGGTCTTCAACAAAGCCCTCCACGACCCCATCGAGAAAACCATCTCTCAAAGCCAAA 682
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QY      1114 AACCAAGTCAAGCTGACCTGCTGCTGGTCAAAAGGCTTCTATCCAGCGACATCGCGTGGAG 1173
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QY      1174 TGGGAGAGCAATGGGAGCCGAGAGAACACTACAGACGACGCTCCCGTCTGGACTCC 1233
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QY      1234 GACGGCTCTCTTCTCTCTACAGCAAGCTCACCGTGGACAAAGAGCAGTGGCAGCAGGG 1293
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QY      1294 AACGTCTTCTCATGCTCCGTCGTCATGAGGCTCTGCACAAACCACTACAGCAGAGAGC 1353
Db      923 AACGTCTTCTCATGCTCCGTCGTCATGAGGCTCTGCACAAACCACTACAGCAGAGAGC 982
QY      1354 CTCTCCCTGTCTCCGGGTAATGA 1377
Db      983 CTCTCCCTGTCTCCGGGTAATGA 1006

RESULT 7
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DEFINITION
ACCESSION CR595172
VERSION   1
KEYWORDS  HTCC; CNSLT; cDNA.
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
          1 (bases 1 to 1048)
          Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
          Full-length cDNA libraries and normalization
          Unpublished
          Contact : Feng Liang Email : fliang@lifetech.com URL :
          http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
          Faraday Avenue
          2 (bases 1 to 1048)
          Genoscope.
          Direct Submission
          Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
          BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
          - Web : www.genoscope.cns.fr)
          1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
          end enriched, double-strand cDNA was digested with Not I and cloned
          into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
          was normalized. Library was constructed by Life Technologies, a
          division of Invitrogen.
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Query Match 49.6%; Score 682.4; DB 3; Length 1048;
Best Local Similarity 99.9%; Pred. No. 1.4e-178;
Matches 683; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      694 GACAAACTCACATGCCACCGTCCGACGACCTGAACCTCTGGGGGACCGTCAGTC 753

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VERSION CR604961.1 GI:50485768
KEYWORDS HTC; CNSLT_CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1. (bases 1 to 1091)
FULL-LENGTH CDNA LIBRARIES AND NORMALIZATION Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
REMARK Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
Genoscope.
2 (bases 1 to 1091)
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
source Location/Qualifiers
1..1091
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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ORIGIN
Query Match 49.6%; Score 682.4; DB 3; Length 1091;
Best Local Similarity 99.9%; Pred. No. 1.4e-178;
Matches 683; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 694 GACAAACTCACATGCCCGTCCAGACCTGAACTCTCGGGGGACCGTCAGTC 753
DB 323 GACAAACTCACATGCCCGTCCAGACCTGAACTCTCGGGGGACCGTCAGTC 382
QY 754 TTCCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTCA 813
DB 383 TTCCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTCA 442
QY 814 TCGGTGGTGGTGCATTAATGCCAAGACAAAGCCGCGGAGGAGCAGTACACAGCAGTAC 873
DB 443 TCGGTGGTGGTGCATTAATGCCAAGACAAAGCCGCGGAGGAGCAGTACACAGCAGTAC 502
QY 874 GCGTGGAGGTGCATTAATGCCAAGACAAAGCCGCGGAGGAGCAGTACACAGCAGTAC 933
DB 503 GCGTGGAGGTGCATTAATGCCAAGACAAAGCCGCGGAGGAGCAGTACACAGCAGTAC 562
QY 934 CGTGTGGTGCAGCTCTCAACCGCTTCGACAGGACTGGCTGAATGGCAAGGATCAAG 993
DB 563 CGTGTGGTGCAGCTCTCAACCGCTTCGACAGGACTGGCTGAATGGCAAGGATCAAG 622
QY 994 TGCAGAGTCTCCAAACAGCCCTCCAGCCCCCATCGAGAAACCATCTCCAAAGCAAA 1053
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DB 683 GGCAGCCCGGAGAACACAGGTGTACACCTCGCCCCCATCGCGGATGAGCTGACCAAG 742
QY 1114 AACAGGTGCAGCTGACCTGCTGGTCAAGAGGCTTCTATCCAGGACATCGCGGTGAG 1173
DB 743 AACAGGTGCAGCTGACCTGCTGGTCAAGAGGCTTCTATCCAGGACATCGCGGTGAG 802
QY 1174 TGGGAGAGCAATGGGAGCGGAGAACCACTACAGACACGCTCCCGTGTGGACTCC 1233
DB 803 TGGGAGAGCAATGGGAGCGGAGAACCACTACAGACACGCTCCCGTGTGGACTCC 862

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QY 1234 GACGGCTCCTTCTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCGGG 1293
DB 863 GACGGCTCCTTCTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCGGG 922
QY 1294 AACGTCTTCTCATGCTCCGTCGATGATGAGCTCTGCACAACCACTACACGCAAGAGC 1353
DB 923 AACGTCTTCTCATGCTCCGTCGATGATGAGCTCTGCACAACCACTACACGCAAGAGC 982
QY 1354 CTCCTCCCTGTCTCCGGGTAATGA 1377
DB 983 CTCCTCCCTGTCTCCGGGTAATGA 1006

RESULT 10
LOCUS CR616804
DEFINITION full-length cDNA clone CS0DI048YC07 of Placenta Cot 25-normalized
of Homo sapiens (human).
ACCESSION CR616804
VERSION CR616804.1 GI:50497611
KEYWORDS HTC; CNSLT_CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS 1 (bases 1 to 1093)
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
REMARK Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1093)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI048YC07"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
ORIGIN
Query Match 49.6%; Score 682.4; DB 3; Length 1093;
Best Local Similarity 99.9%; Pred. No. 1.4e-178;
Matches 683; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 694 GACAAACTCACATGCCCGTCCAGACCTGAACTCTCGGGGGACCGTCAGTC 753
DB 323 GACAAACTCACATGCCCGTCCAGACCTGAACTCTCGGGGGACCGTCAGTC 382
QY 754 TTCCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTCA 813
DB 383 TTCCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTCA 442
QY 814 TCGGTGGTGGTGCATTAATGCCAAGACAAAGCCGCGGAGGAGCAGTACACAGCAGTAC 873
DB 443 TCGGTGGTGGTGCATTAATGCCAAGACAAAGCCGCGGAGGAGCAGTACACAGCAGTAC 502
QY 874 GCGTGGAGGTGCATTAATGCCAAGACAAAGCCGCGGAGGAGCAGTACACAGCAGTAC 933
DB 503 GCGTGGAGGTGCATTAATGCCAAGACAAAGCCGCGGAGGAGCAGTACACAGCAGTAC 562

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REFERENCE 2 (bases 1 to 1100)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES Location/Qualifiers
source 1..1100
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="CS0D1081YF02"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
ORIGIN
Query Match 49.6%; Score 682.4; DB 3; Length 1100;
Best Local Similarity 99.9%; Pred. No. 1.4e-178;
Matches 683; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 694 GACAAACTCACATGCCCGTGCACAGCACCTGAACTCTGGGGGACCGTCAGTC 753
DB 319 GACAAACTCACATGCCCGTGCACAGCACCTGAACTCTGGGGGACCGTCAGTC 378
QY 754 TTCCTCTTCCCGCCAAACCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTCA 813
DB 379 TTCCTCTTCCCGCCAAACCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTCA 438
QY 814 TGGTGGAGTGTGATTAATGCAAGACCAAGCCCGGAGGAGGAGTACAAACAGCAGTAC 933
DB 439 TGGTGGAGTGTGATTAATGCAAGACCAAGCCCGGAGGAGGAGTACAAACAGCAGTAC 558
QY 934 GCGTGGAGTGTGATTAATGCAAGACCAAGCCCGGAGGAGGAGTACAAACAGCAGTAC 993
DB 559 GCGTGGAGTGTGATTAATGCAAGACCAAGCCCGGAGGAGGAGTACAAACAGCAGTAC 618
QY 994 TGCAGAGTCTCCAACAAAGCCCTCCAGGCCCCCATCGAGAAAACCATCTCCAAAGCCAA 1053
DB 619 TGCAGAGTCTCCAACAAAGCCCTCCAGGCCCCCATCGAGAAAACCATCTCCAAAGCCAA 678
QY 1054 GGCAGCCCGGAGAACCAAGGTGTACACCTGCCCGCCCATCCCGGATGAGCTGACCAAG 1113
DB 679 GGCAGCCCGGAGAACCAAGGTGTACACCTGCCCGCCCATCCCGGATGAGCTGACCAAG 738
QY 1114 AACAGGTGAGCTGAGTCTGCTGGTCAAGAGTCTTATCCAGCAGCATTCGCGGTGGAG 1173
DB 739 AACAGGTGAGCTGAGTCTGCTGGTCAAGAGTCTTATCCAGCAGCATTCGCGGTGGAG 798
QY 1174 TGGGAGAGCAATGGGAGCGGAGAACACTACAGACCAAGCCCTCCCGTGGAGTCC 1233
DB 799 TGGGAGAGCAATGGGAGCGGAGAACACTACAGACCAAGCCCTCCCGTGGAGTCC 858
QY 1234 GACGGTCTCTTCTCTTCTACAGCAAGCTCACCGTGGAGAGAGGTGGCAGAGGGG 1293
DB 859 GACGGTCTCTTCTCTTCTACAGCAAGCTCACCGTGGAGAGAGGTGGCAGAGGGG 918
QY 1294 AACGTCTTCTATGCTCCGATGATGAGGTCTGCACAAACCATCTACAGCAAGAGAGC 1353
DB 919 AACGTCTTCTATGCTCCGATGATGAGGTCTGCACAAACCATCTACAGCAAGAGAGC 978
QY 1354 CTCTCCCTGTCTCCGGTAAATGA 1377
DB 979 CTCTCCCTGTCTCCGGTAAATGA 1002
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RESULT 13
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LOCUS full-length cDNA clone CS0CAP008YF07 of Thymus of Homo sapiens
DEFINITION (human).
ACCESSION CR601777
VERSION GI:50482584
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1102)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polaves, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1102)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES Location/Qualifiers
source 1..1102
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0CAP008YF07"
/tissue_type="Thymus"
/plasmid="pCMVSPORT_6"
ORIGIN
Query Match 49.6%; Score 682.4; DB 3; Length 1102;
Best Local Similarity 99.9%; Pred. No. 1.4e-178;
Matches 683; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 694 GACAAACTCACATGCCCGTGCACAGCACCTGAACTCTGGGGGACCGTCAGTC 753
DB 319 GACAAACTCACATGCCCGTGCACAGCACCTGAACTCTGGGGGACCGTCAGTC 378
QY 754 TTCCTCTTCCCGCCAAACCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTCA 813
DB 379 TTCCTCTTCCCGCCAAACCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTCA 438
QY 814 TGGTGGTGGAGCGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGAC 873
DB 439 TGGTGGTGGAGCGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGAC 498
QY 874 GCGTGGAGTGTGATTAATGCAAGACCAAGCCCGGAGGAGGAGTACAAACAGCAGTAC 933
DB 499 GCGTGGAGTGTGATTAATGCAAGACCAAGCCCGGAGGAGGAGTACAAACAGCAGTAC 558
QY 934 CGTGTGGTGTGAGTGTGATTAATGCAAGACCAAGCCCGGAGGAGTACAAACAGCAGTAC 993
DB 559 CGTGTGGTGTGAGTGTGATTAATGCAAGACCAAGCCCGGAGGAGTACAAACAGCAGTAC 618
QY 994 TGCAGAGTCTCCAACAAAGCCCTCCAGGCCCCCATCGAGAAAACCATCTCCAAAGCCAA 1053
DB 619 TGCAGAGTCTCCAACAAAGCCCTCCAGGCCCCCATCGAGAAAACCATCTCCAAAGCCAA 678
QY 1054 GGCAGCCCGGAGAACCAAGGTGTACACCTGCCCGCCCATCCCGGATGAGCTGACCAAG 1113
DB 679 GGCAGCCCGGAGAACCAAGGTGTACACCTGCCCGCCCATCCCGGATGAGCTGACCAAG 738
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QY 1114 AACGAGTCTGACCTGACCTGCTGCTCAAGAGCTTCTATCCAGCGACATCCCGTGGAG 1173
Db |||||||
QY 739 AACGAGTCTGACCTGACCTGCTGCTCAAGAGCTTCTATCCAGCGACATCCCGTGGAG 798
Db |||||||
QY 1174 TGGGAGCAATGGGAGCGGAGAGAACTACAAGACCAACGCTCCCGTGTGGAAGTCC 1233
Db |||||||
QY 1234 GACGGCTCTTCTTCTTACAGCAAGTCAACGCTGGAACAAGACAGGTGGGAGAGGG 1293
Db |||||||
QY 859 GACGGCTCTTCTTCTTACAGCAAGTCAACGCTGGAACAAGACAGGTGGGAGAGGG 918
QY 1294 AACGCTCTCTGATGCTGCTGATGATGAGGCTCTGCAACCACTACACGAGAGAGC 1353
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QY 1354 CTCTCCCTGCTCCCGGTAATGA 1377
Db |||||||
QY 979 CTCTCCCTGCTCCCGGTAATGA 1002
Db |||||||

RESULT 14
CR625051 1102 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CS0DI059YL06 of Placenta Cot 25-normalized
DEFINITION of Homo sapiens (human).
ACCESSION CR625051
VERSION CR625051.1 GI:50505858
KEYWORDS HTC; CNSLT cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1102)
AUTHORS Li, W. B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
Genoscope.
2 (bases 1 to 1102)
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
source Location/Qualifiers
1 .1102
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ORIGIN
Query Match 49.6%; Score 682.4; DB 3; Length 1102;
Best Local Similarity 99.9%; Pred. No. 1.4e-178;
Matches 683; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 694 GACAAACTCACATGCCACCGTCCCGAGACCTGAACTCTGGGGGACCGTCAAGTC 753
Db |||||||
QY 323 GACAAACTCACATGCCACCGTCCCGAGACCTGAACTCTGGGGGACCGTCAAGTC 382
QY 754 TTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTCA 813
Db |||||||
QY 383 TTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTCA 442

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QY 814 TCGTGTGGTGGAGCGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGAC 873
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QY 443 TCGTGTGGTGGAGCGTGAGCCACGAAGACCTGAGGTCAAGTTCAACTGGTACGTGGAC 502
Db |||||||
QY 874 GCGGTGGAGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAAACGACGTAC 933
Db |||||||
QY 503 GCGGTGGAGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAAACGACGTAC 562
QY 934 CTTGTGGTTCAGCGTCTCTACCGTCTCTGACAGGACTGGCTGAATGGCAAGAGTACAAG 993
Db |||||||
QY 563 CTTGTGGTTCAGCGTCTCTACCGTCTCTGACAGGACTGGCTGAATGGCAAGAGTACAAG 622
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Db |||||||
QY 623 TGCAGAGTCTCAACAAAGAGCCCTCCAGCCGCCATCGAGAAACCATCTCCAAAGCCAA 682
QY 1054 GGGCAGCCCGGAGAAACACAGGTGTACACCTGCCCCCATCCCGGATGAGTGCACAAAG 1113
Db |||||||
QY 683 GGGCAGCCCGGAGAAACACAGGTGTACACCTGCCCCCATCCCGGATGAGTGCACAAAG 742
QY 1114 AACGAGTCTGACCTGACCTGCTGCTCAAGAGCTTCTATCCAGCGACATCCCGTGGAG 1173
Db |||||||
QY 743 AACGAGTCTGACCTGACCTGCTGCTCAAGAGCTTCTATCCAGCGACATCCCGTGGAG 802
QY 1174 TGGGAGCAATGGGAGCGGAGAGCACTACAAGACCAACGCTCCCGTGTGGAAGTCC 1233
Db |||||||
QY 803 TGGGAGCAATGGGAGCGGAGAGCACTACAAGACCAACGCTCCCGTGTGGAAGTCC 862
QY 1234 GACGGCTCTTCTTCTTCTTACAGCAAGTCAACGCTGGGAGCAAGAGCAGGTGGGAGGG 1293
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QY 863 GACGGCTCTTCTTCTTCTTACAGCAAGTCAACGCTGGGAGCAAGAGCAGGTGGGAGGG 922
QY 1294 AACGCTCTTCTATGCTCCGCTGATGATGAGGCTCTGCAACCACTACACGAGAGAGC 1353
Db |||||||
QY 923 AACGCTCTTCTATGCTCCGCTGATGATGAGGCTCTGCAACCACTACACAGAGAGC 982
QY 1354 CTCTCCCTGCTCCCGGTAATGA 1377
Db |||||||
QY 983 CTCTCCCTGCTCCCGGTAATGA 1006
Db |||||||

RESULT 15
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LOCUS full-length cDNA clone CS0DE010YH13 of Placenta of Homo sapiens
DEFINITION (human).
ACCESSION CR595194
VERSION CR595194.1 GI:50476001
KEYWORDS HTC; CNSLT cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1103)
AUTHORS Li, W. B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
Genoscope.
2 (bases 1 to 1103)
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
source Location/Qualifiers
1 .1103

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ORIGIN

Query Match		49.6%;	Score 682.4;	DB 3;	Length 1103;
Best Local Similarity		99.9%;	Pred. No. 1.4e-178;		
Matches	683;	Conservative	0;	Mismatches	1; Indels 0; Gaps 0;
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Qy	754	TTCTCTTCCCCCAAAACCCAAAGGACACCTCATGATCTCCCGGACCCCTGAGGTCACA	813		
Db	379	TTCTCTTCCCCCAAAACCCAAAGGACACCTCATGATCTCCCGGACCCCTGAGGTCACA	438		
Qy	814	TGCGTGGTGGTGACGTGAGCCACGAGACCCCTGAGGTCAAAGTTCAACTGGTACGTGGAC	873		
Db	439	TGCGTGGTGGTGACGTGAGCCACGAGACCCCTGAGGTCAAAGTTCAACTGGTACGTGGAC	498		
Qy	874	GGCGTGGAGGTGCATTAATGCAAGACAAAGCCCGGAGGAGCAGTACAAACAGCACGTAC	933		
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Qy	934	CGTGTGGTCAGCGTCTCACCCTCCCTGACACGAGGACTGGCTGAATGGCAAGGATACAAG	993		
Db	559	CGTGTGGTCAGCGTCTCACCCTCCCTGACACGAGGACTGGCTGAATGGCAAGGATACAAG	618		
Qy	994	TGCAAGGTCTCCAAACAAAGCCCTCCAGACCCCTCGAGAAACCATCTCCAAAGCCAAA	1053		
Db	619	TGCAAGGTCTCCAAACAAAGCCCTCCAGACCCCTCGAGAAACCATCTCCAAAGCCAAA	678		
Qy	1054	GGGAGCCCGGAGAACCAACAGGTGTACACCTGCCCCCATCCCGGATGAGCTGACCAAG	1113		
Db	679	GGGAGCCCGGAGAACCAACAGGTGTACACCTGCCCCCATCCCGGATGAGCTGACCAAG	738		
Qy	1114	AACAGGTGAGCTGACCTGCTGCTCAAGGCTTCTATCCAGCGACATCGCCGTGGAG	1173		
Db	739	AACAGGTGAGCTGACCTGCTGCTCAAGGCTTCTATCCAGCGACATCGCCGTGGAG	798		
Qy	1174	TGGGAGCAATGGGAGCGCGGAGAACAACTACAAGACACGCTCCCGTGTGGACTCC	1233		
Db	799	TGGGAGCAATGGGAGCGCGGAGAACAACTACAAGACACGCTCCCGTGTGGACTCC	858		
Qy	1234	GACGGCTCTTCTTCTTACAGCAAGCTCACCGTGACAAGACAGGTGGCAGCAGGGG	1293		
Db	859	GACGGCTCTTCTTCTTACAGCAAGCTCACCGTGACAAGACAGGTGGCAGCAGGGG	918		
Qy	1294	AAGCTTCTCATGCTCCGTGATGATGAGGCTCTGCACAACTACACGCAAGAGAGC	1353		
Db	919	AAGCTTCTCATGCTCCGTGATGATGAGGCTCTGCACAACTACACGCAAGAGAGC	978		
Qy	1354	CTCTCCCTGCTCCCGGGTAAATGA	1377		
Db	979	CTCTCCCTGCTCCCGGGTAAATGA	1002		

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Job time : 4305 secs

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OM nucleic - nucleic search, using sw model

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8345.011 Million cell updates/sec

Title: US-10-811-170-1

Perfect score: 1377

Sequence: 1 atggcagctactgggacac.....ccctgtctcgggtaaatga 1377

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2\_6/prodata/1/ina/5B COMB.seq.\*
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- 6: /cgn2\_6/prodata/1/ina/backfile1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	1039	75.0	1359	4	US-09-773-877B-15
5	1032.4	75.0	1389	4	US-09-773-877B-17
6	987.4	71.7	1674	4	US-09-773-877B-13
7	982.4	71.3	1704	4	US-09-773-877B-19
8	980.8	71.2	1704	4	US-09-773-877B-11
9	686	49.8	2043	3	US-08-227-496C-14
10	684	49.7	705	4	US-09-023-655-1223
11	684	49.7	1019	3	US-09-178-869-1
12	684	49.7	1019	4	US-09-761-413-1
13	684	49.7	1182	3	US-09-180-100-18
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15	684	49.7	1428	2	US-08-634-223-19
16	684	49.7	1428	2	US-08-634-224-19
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30	684	49.7	1437	4	US-09-526-098-7	Sequence 7, Appl
31	684	49.7	1437	4	US-09-383-916-7	Sequence 7, Appl
32	684	49.7	1458	4	US-08-030-175-6	Sequence 6, Appl
33	684	49.7	1458	4	US-08-030-175-7	Sequence 7, Appl
34	684	49.7	1467	4	US-08-030-175-5	Sequence 5, Appl
35	684	49.7	1494	4	US-09-499-846-5	Sequence 3, Appl
36	684	49.7	1578	4	US-09-499-846-3	Sequence 3, Appl
37	684	49.7	1599	4	US-09-023-655-1120	Sequence 1120, Ap
38	684	49.7	1617	2	US-08-378-939-9	Sequence 9, Appl
39	684	49.7	1720	4	US-09-746-359A-52	Sequence 52, Appl
40	684	49.7	1869	4	US-09-499-846-1	Sequence 1, Appl
41	684	49.7	3477	4	US-09-313-942-25	Sequence 25, Appl
42	684	49.7	3507	4	US-09-313-942-23	Sequence 23, Appl
43	684	49.7	9209	1	US-08-149-099C-3	Sequence 3, Appl
44	684	49.7	9209	1	US-08-476-275-2	Sequence 2, Appl
45	684	49.7	9209	2	US-08-478-967A-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1

US-09-773-877B-25  
; Sequence 25, Application US/09773877B  
; Patent No. 6833349

; GENERAL INFORMATION:

; APPLICANT: Xia, Yu-Ping et al.

; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES

; FILE REFERENCE: REG 710b

; CURRENT APPLICATION NUMBER: US/09/773,877B

; CURRENT FILING DATE: 2001-01-31

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 25

; LENGTH: 1377

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: VEGFR1R2.FcdeltaC1(a) Receptor

; NAME/KEY: CDS

; LOCATION: (1)..(1377)

US-09-773-877B-25

Query Match	100.0%;	Score 1377;	DB 4;	Length 1377;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1377;	Conservative	0;	Mismatches	0;
			Indels	0;
Gaps				0;
QY	1	ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGCTGGCGGCTGCTCAGCTGCTGCTTCTC	60	
DB	1	ATGGTCAGCTACTGGGACACCGGGGTCCTGCTGCTGGCGGCTGCTCAGCTGCTGCTTCTC	60	
QY	61	ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTTCGTAGAGATGTACAGTGAATC	120	
DB	61	ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTTCGTAGAGATGTACAGTGAATC	120	
QY	121	CCCGAAATATACACATGACTGAAGGAGGAGCTCGTCAATTCCTGCCGGGTACCTCA	180	
DB	121	CCCGAAATATACACATGACTGAAGGAGGAGCTCGTCAATTCCTGCCGGGTACCTCA	180	
QY	181	CCTAACATCACTGTTACTTTAAAAAGTTTCCACTTTGACACTTTGATCCCTGATGGAATA	240	
DB	181	CCTAACATCACTGTTACTTTAAAAAGTTTCCACTTTGACACTTTGATCCCTGATGGAATA	240	
QY	241	CGCATTAATCTGGGACAGTGAAGGCGCTCATCATATCAAAATGCAAGTCAAGAAATA	300	
DB	241	CGCATTAATCTGGGACAGTGAAGGCGCTCATCATATCAAAATGCAAGTCAAGAAATA	300	
QY	301	GGGCTTCTGACCTGTGAAGCAAGTCAATGGGCATTTGTATGAACAACACTATCTCACA	360	
DB	301	GGGCTTCTGACCTGTGAAGCAAGTCAATGGGCATTTGTATGAACAACACTATCTCACA	360	

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QY 361 CATCGAACAACCAATACATCATAGATGGTTCTGAGTCCGCTCTCATGGAATTGAACATA 420
Db 361 CATCGAACAACCAATACATCATAGATGGTTCTGAGTCCGCTCTCATGGAATTGAACATA 420
QY 421 TCTGTTGGAGAAAAGCTTGCTTAAATTTGTACAGCAAGAACTGAACCTAAATGTGGGATT 480
Db 421 TCTGTTGGAGAAAAGCTTGCTTAAATTTGTACAGCAAGAACTGAACCTAAATGTGGGATT 480
QY 481 GACTTCAACTGGGAATACCTCTTCCGAAGCATCAGCATAAGAAACTTTGTAACCGAGAC 540
Db 481 GACTTCAACTGGGAATACCTCTTCCGAAGCATCAGCATAAGAAACTTTGTAACCGAGAC 540
QY 541 CTAATAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGGAGCACTTAACATATAGATGT 600
Db 541 CTAATAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGGAGCACTTAACATATAGATGT 600
QY 601 GTAACCCGGAGTGACCAAGGATTTACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660
Db 601 GTAACCCGGAGTGACCAAGGATTTACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660
QY 661 AAGAACAGACATTTCTCAGGGTCCATGAAGGACAAAACCTACACATGCCACCGTGC 720
Db 661 AAGAACAGACATTTCTCAGGGTCCATGAAGGACAAAACCTACACATGCCACCGTGC 720
QY 721 CCAGCACCTGAACCTCTGGGGGACCGTCAGTCTTCTCTCCCCCAAAACCCCAAGGAC 780
Db 721 CCAGCACCTGAACCTCTGGGGGACCGTCAGTCTTCTCTCCCCCAAAACCCCAAGGAC 780
QY 781 ACCCTCATGATCTCCGGGACCCCTGAGGTACATGCGTGGTGGTGACGTGAGCCACGAA 840
Db 781 ACCCTCATGATCTCCGGGACCCCTGAGGTACATGCGTGGTGGTGACGTGAGCCACGAA 840
QY 841 GACCCCTGAGTCAAGTTCAACTGTTGAGTGGACGCGGTGAGGTGCAATATGCCAAGACA 900
Db 841 GACCCCTGAGTCAAGTTCAACTGTTGAGTGGACGCGGTGAGGTGCAATATGCCAAGACA 900
QY 901 AAGCCGGGGAGGAGCAGTACACAGCAGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGG 960
Db 901 AAGCCGGGGAGGAGCAGTACACAGCAGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGG 960
QY 961 CACCGAGCTGGCTGAATGCAAGGAGTACAGTGCAGGTCTCCAAAGGAGGAGGAGGAGGAG 1020
Db 961 CACCGAGCTGGCTGAATGCAAGGAGTACAGTGCAGGTCTCCAAAGGAGGAGGAGGAGGAG 1020
QY 1021 GCGCCCATCGAGAAAACCATCTCCAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
Db 1021 GCGCCCATCGAGAAAACCATCTCCAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
QY 1081 ACCCTGCCCCCATCCCGGATGAGCTGACCAAGAACCCAGTCCAGTCCAGTCCAGTCCAGT 1140
Db 1081 ACCCTGCCCCCATCCCGGATGAGCTGACCAAGAACCCAGTCCAGTCCAGTCCAGTCCAGT 1140
QY 1141 AAAGGCTTCTATCCAGCAGCATCGCGTGGAGTGGAGAGCAATGGGAGGAGGAGGAGGAGGAG 1200
Db 1141 AAAGGCTTCTATCCAGCAGCATCGCGTGGAGTGGAGAGCAATGGGAGGAGGAGGAGGAGGAG 1200
QY 1201 AACTACAAGACCAAGCTCCCGTGGTGGACTCCGAGGGTCTCTCTCTCTCTCTCTCTCTCTCT 1260
Db 1201 AACTACAAGACCAAGCTCCCGTGGTGGACTCCGAGGGTCTCTCTCTCTCTCTCTCTCTCTCT 1260
QY 1261 CTCACCGTGGACAGAGCAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1320
Db 1261 CTCACCGTGGACAGAGCAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1320
QY 1321 GAGGCTCTGCACACCACTACAGCAGAGAGAGGCTCTCCCTGTCTCCGGGTAAATGA 1377
Db 1321 GAGGCTCTGCACACCACTACAGCAGAGAGAGGCTCTCCCTGTCTCCGGGTAAATGA 1377
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RESULT 2

US-09-773-877B-21

; Sequence 21, Application US/09773877B

; Patent No. 6833349

```
; GENERAL INFORMATION:
; APPLICANT: Xia, Yu-ping et al.
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
; FILE REFERENCE: REG 710b
; CURRENT APPLICATION NUMBER: US/09/773,877B
; CURRENT FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 21
; LENGTH: 1453
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fli1D2.Fli1D3.Fdel1aC1(a)Receptor
; NAME/KEY: CDS
; LOCATION: (69)..(1442)
US-09-773-877B-21
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Query Match 96.5%; Score 1328.4; DB 4; Length 1453;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 1367; Conservative 0; Mismatches 1; Indels 18; Gaps 2;

QY 1 ATGGTCAGCTACTGGGACACCGGGTCCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60
Db 69 ATGGTCAGCTACTGGGACACCGGGTCCCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 128
QY 61 ACAGGATCTAGTTCGGGAAGTGATACCGGTAGACCTTTTCGTAGAGATGTACAGTGAATC 120
Db 129 ACAGGATCTAGTTCGGGA-----GGTAGACCTTTTCGTAGAGATGTACAGTGAATC 179
QY 121 CCCGAATATACATGACTGAAGGAGGAGCTCGTCAATTCCTGCGGGTTAGTCA 180
Db 180 CCCGAATATACATGACTGAAGGAGGAGCTCGTCAATTCCTGCGGGTTAGTCA 239
QY 181 CCTAACATCACTGTTACTTTAAAGTTCACATTGACACTTTGATCCCTGATGAAAA 240
Db 240 CCTAACATCACTGTTACTTTAAAGTTCACATTGACACTTTGATCCCTGATGAAAA 299
QY 241 CGCATAATCTGGGACAGTAGAAGGCTTCATCATATCAAAATGCAACGTACAAAGAAATA 300
Db 300 CGCATAATCTGGGACAGTAGAAGGCTTCATCATATCAAAATGCAACGTACAAAGAAATA 359
QY 301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGCATTTGTATAGCAACAATATCTCA 360
Db 360 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGCATTTGTATAGCAACAATATCTCA 419
QY 361 CATCGAACAACAATACATCATAGATGGTTCCTGAGTCCGCTCTCATGGAATTGAACATA 420
Db 420 CATCGAACAACAATACATCATAGATGGTTCCTGAGTCCGCTCTCATGGAATTGAACATA 479
QY 421 TCTGTTGGAGAAAAGCTTGCTTAAATTTGTAAGCAAGAACTGAACCTAAATGTGGGATT 480
Db 480 TCTGTTGGAGAAAAGCTTGCTTAAATTTGTAAGCAAGAACTGAACCTAAATGTGGGATT 539
QY 481 GACTTCAACTGGGAATACCTCTTCCGAGCATCAGCATAAGAACTTTGTAACCGAGAC 540
Db 540 GACTTCAACTGGGAATACCTCTTCCGAGCATCAGCATAAGAACTTTGTAACCGAGAC 599
QY 541 CTAATAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGGAGCACTTAACATATAGATGT 600
Db 600 CTAATAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGGAGCACTTAACATATAGATGT 659
QY 601 GTAACCCGGAGTGACCAAGGATTTACCTGTGAGCATCCAGTGGGCTGATGACCAAG 660
Db 660 GTAACCCGGAGTGACCAAGGATTTACCTGTGAGCATCCAGTGGGCTGATGACCAAG 719
QY 661 AAGAACAGACATTTGTCTCAGGGTCCATGAAAG-----GACAAAACTCACACATGC 711
Db 720 AAGAACAGACATTTGTCTCAGGGTCCATGAAAGGGGCGCGGCGACAAAACCTCACACATGC 779
QY 712 CCACCGTGCCAGCACCTGAACTCTCTGGGGGAGCCGTGAGTCTTCTCTTCCCCCAAAA 771
Db 780 CCACCGTGCCAGCACCTGAACTCTCTGGGGGAGCCGTGAGTCTTCTCTTCCCCCAAAA 839
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Db 1131 CAGGTGTACACCCCTGCCCCATCCCGGATGAGTGAACCAAGACCCAGGTACGCTGACC 1190  
QY 1132 TGCCTGGTCAAGGCTTCTATCCAGCAGATGCGCGTGGAGTGAGGAGCAATGGGCAG 1191  
Db 1191 TGCCTGGTCAAGGCTTCTATCCAGCAGATGCGCGTGGAGTGAGGAGCAATGGGCAG 1250  
QY 1192 CCGGAGAACAACTACAAGACCAAGCCTCCCGTGTGGAGTCCGAGCGGCTCTTCTTCCTC 1251  
Db 1251 CCGGAGAACAACTACAAGACCAAGCCTCCCGTGTGGAGTCCGAGCGGCTCTTCTTCCTC 1310  
QY 1252 TACAGCAAGCTCACCGTGGACAAGAGCAGTGGCAGCAGGGAAAGCTCTTCTCATGCTCC 1311  
Db 1311 TATAGCAAGCTCACCGTGGACAAGAGCAGTGGCAGCAGGGAAAGCTCTTCTCATGCTCC 1370  
QY 1312 GTGATGCATGAGCTCTGCACAAACCACTACACGAGAGAGCCTCTCCCTGTCTCGGGT 1371  
Db 1371 GTGATGCATGAGCTCTGCACAAACCACTACACGAGAGAGCCTCTCCCTGTCTCGGGT 1430  
QY 1372 AAATGA 1377  
Db 1431 AAATGA 1436

## RESULT 4

US-09-773-877B-15  
; Sequence 15, Application US/09773877B  
; Patent No. 6833349  
; GENERAL INFORMATION:  
; APPLICANT: Xia, Yu-Ping et al.  
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES  
; FILE REFERENCE: REG 710b  
; CURRENT APPLICATION NUMBER: US/09/773,877B  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 15  
; LENGTH: 1359  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Flt1(2-3 deltaB) -Fc (Mut2)  
; NAME/KEY: CDS  
; LOCATION: (1)...(1359)  
US-09-773-877B-15

Query Match 75.5%; Score 1039; DB 4; Length 1359;  
Best Local Similarity 86.3%; Pred. No. 3.5e-268;  
Matches 1189; Conservative 0; Mismatches 170; Indels 18; Gaps 3;

QY 1 ATGGTCAGCTACTGGGACACCGGGTCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60  
Db 1 ATGGTCAGCTACTGGGACACCGGGTCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60  
QY 61 ACAGGATCTAGTTCGGAAGTGATACCGGTAGACCTTTCTGTAGAGATGTACAGTGAATC 120  
Db 61 ACAGGATCTAGTTCGGA-----GGTAGACCTTTCTGTAGAGATGTACAGTGAATC 111  
QY 121 CCGAAATATACATGATGAAGGAGGAGCTGCTCATTCCTGCGGGTTACGTCA 180  
Db 112 CCGAAATATACATGATGAAGGAGGAGCTGCTCATTCCTGCGGGTTACGTCA 171  
QY 181 CCTACATCACTGTTACTTTAAAGATTTCCACTTGACACTTGTATCCCTGATGGAATA 240  
Db 172 CTTAATCACTGTTACTTTAAAGATTTCCACTTTGACACTTTGATCCCTGATGGAATA 231  
QY 241 CGCATAATCTGGGACAGTAGTAAGAGGCTTCATCATATCAATCAATGCAACGTACAAAGAAATA 300  
Db 232 CGCATAATCTGGGACAGTAGTAAGAGGCTTCATCATATCAATGCAACGTACAAAGAAATA 291  
QY 301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAATATCTCACA 360  
Db 292 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAATATCTCACA 351

## RESULT 5

US-09-773-877B-17  
; Sequence 17, Application US/09773877B  
; Patent No. 6833349



; GENERAL INFORMATION:		
; APPLICANT: Xia, Yu-Ping et al.		
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES		
; FILE REFERENCE: REG 710b		
; CURRENT APPLICATION NUMBER: US/09/773,877B		
; CURRENT FILING DATE: 2001-01-31		
; NUMBER OF SEQ ID NOS: 27		
; SOFTWARE: PatentIn version 3.0		
; SEQ ID NO 17		
; LENGTH: 1389		
; TYPE: DNA		
; ORGANISM: Artificial Sequence		
; FEATURE:		
; OTHER INFORMATION: Flt1(2-3)-Fc (Mut3)		
; NAME/KEY: CDS		
; LOCATION: (1)..(1389)		
US-09-773-877B-17		
Query Match		75.0%; Score 1032.4; DB 4; Length 1389;
Best Local Similarity		85.5%; Pred. No. 2.1e-266;
Matches 1201; Conservative		0; Mismatches 161; Indels 42; Gaps 3;
QY	1	ATGGTCAGCTACTGGGACACCGGGGCTCTGCTGGCGGCTGCTCAGCTGTCTGCTTCTC 60
DB	1	ATGGTCAGCTACTGGGACACCGGGGCTCTGCTGGCGGCTGCTCAGCTGTCTGCTTCTC 60
QY	61	ACAGGATCTAGTTCCGGAGTGATACCGGTAGACCTTTTCGTAGAGATGTACAGTGAATC 120
DB	61	ACAGGATCTAGTTCCGGA-----GGTAGACCTTTTCGTAGAGATGTACAGTGAATC 111
QY	121	CCGAAATATTACATGACTGAAGGAAGGAGCTCGTCAATCCCTGCCGGGTTACGTCA 180
DB	112	CCGAAATATTACATGACTGAAGGAAGGAGCTCGTCAATCCCTGCCGGGTTACGTCA 171
QY	181	CCTAACATCACTGTTACTTTAAAAAGTTTCCACTTGACACTTTGATCCCTGATGAAAA 240
DB	172	CCTAACATCACTGTTACTTTAAAAAGTTTCCACTTTGACACTTTGATCCCTGATGAAAA 231
QY	241	CGATAATCTGGACAGTAGAAGGGCTTCATCATATCAATCAATCAATCAATCAATCAAT 300
DB	232	CGATAATCTGGACAGTAGAAGGGCTTCATCATATCAATCAATCAATCAATCAATCAAT 291
QY	301	GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAGACAACTATCTCACA 360
DB	292	GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAGACAACTATCTCACA 351
QY	361	CATCGAACAACCAATCAATCATAGATGGTCTGAGTCCGTCTCATGGAATGAACTA 420
DB	352	CATCGAACAACCAATCAATCATAGATGGTCTCAAAATAAGCACACACCGCCAGTCAAAATTA 411
QY	421	TCTGTTGGAGAAAGCTTGCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGATT 480
DB	412	CTTAGAGGCATACTCTTGCTCAATTTGCTGCTACCTCCCTTTGAACACGAGATT 471
QY	481	GACTTCAACTGGGAATACCCCTTCTCGAAGCATCAGCATAGAAGAACTTGTAAACCGGAG 540
DB	472	CAAATGACCTGGAGTTTACCT-----GATGAAAAAATAAGAGAGCTCCCGTAAGCGCA 525
QY	541	CTHAAACCCAGTCTGGGAGTAGATGAGAAATTTTGTAGCACTTAACTATAGATGGT 600
DB	526	CGAAITGACCAAGCAATTTCCCATGCCAACATATCTACAGTGTCTTACTATTGCAAA 585
QY	601	GTAACCCGGAGTGACCAAGATTGTACACTGTGCAGCATCCAGTGGGTGATGACCAAG 660
DB	586	ATCGAACAACCAAGCAAGACTTTTACTTGTGTGTAAGGAGTGACCATCAATTCAA 645
QY	661	AAGAACAGCACATTTGTGAGGGTCCATGAAAA-----G 693
DB	646	TCGTGTTAACACCTCAGTGCATATATATGATAAGCAGGCCCGGGCGGCCCAATCTGT 705
QY	694	GACAAACTCACATGCCACCGTGCACGACCTGAACTCTCTGGGGGACCGTCAGTC 753
DB	706	GACAAACTCACATGCCACCGTGCACGACCTGAACTCTCTGGGGGACCGTCAGTC 765
QY	754	TTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTCA 813
DB	766	TTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTCA 825
QY	814	TGCGTGGTGGACCTGAGCCACGAAGACCTTGAGGTCAAGTTCAACTGGTACGTGGAC 873
DB	826	TGCGTGGTGGACCTGAGCCACGAAGACCTTGAGGTCAAGTTCAACTGGTACGTGGAC 885
QY	874	GGCGTGGAGGTGCATAATGCCAAGCAAAAGCCGCGGAGGAGCAGTACACACGACCTAC 933
DB	886	GGCGTGGAGGTGCATAATGCCAAGCAAAAGCCGCGGAGGAGCAGTACAAACGACCTAC 945
QY	934	CGTGTGGTCAAGCGTCTCCACCGTCTGCACACGAGACTGGCTGAATGGCAAGGATCAAG 993
DB	946	CGTGTGGTCAAGCGTCTCCACCGTCTGCACACGAGACTGGCTGAATGGCAAGGATCAAG 1005
QY	994	TGCAAGGTCTCCAAAGAGCCCTCCAGCCCTCCAGCCCTCCAGAGAAACCATCTCCAAAGCCAAA 1053
DB	1006	TGCAAGGTCTCCAAAGAGCCCTCCAGCCCTCCAGCCCTCCAGAGAAACCATCTCCAAAGCCAAA 1065
QY	1054	GGGACGCCCCGAGAACACAGGTGTACACCTGCCCCCATCCCGGATGAGCTGACCAAG 1113
DB	1066	GGGACGCCCCGAGAACACAGGTGTACACCTGCCCCCATCCCGGATGAGCTGACCAAG 1125
QY	1114	AACAGGTGAGCTGACCTGCTGCTGCTCAAGGGCTTCTATCCACGACATCGCGGTGGAG 1173
DB	1126	AACAGGTGAGCTGACCTGCTGCTGCTCAAGGGCTTCTATCCACGACATCGCGGTGGAG 1185
QY	1174	TGGGAGAGCAATGGGCGAGCGGAGAAACAACTACAAGACCAACGCTCCCGTGGACTCC 1233
DB	1186	TGGGAGAGCAATGGGCGAGCGGAGAAACAACTACAAGACCAACGCTCCCGTGGACTCC 1245
QY	1234	GAGGCTCTCTTCTCTCTACAGCAAGCTCACCGTGGACAAAGAGAGTGGCAGCAGGG 1293
DB	1246	GAGGCTCTCTTCTCTCTACAGCAAGCTCACCGTGGACAAAGAGAGTGGCAGCAGGG 1305
QY	1294	AACGTCTTCTCATGCTCCGTGATGATGAGGCTCTGCACAAACCACTACACGCAAGAGC 1353
DB	1306	AACGTCTTCTCATGCTCCGTGATGATGAGGCTCTGCACAAACCACTACACGCAAGAGC 1365
QY	1354	CTCTCCCTGTCTCCGGGTAAATGA 1377
DB	1366	CTCTCCCTGTCTCCGGGTAAATGA 1389
RESULT 6		
US-09-773-877B-13		
; Sequence 13, Application US/09773877B		
; Patent No. 6833349		
; GENERAL INFORMATION:		
; APPLICANT: Xia, Yu-Ping et al.		
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES		
; FILE REFERENCE: REG 710b		
; CURRENT APPLICATION NUMBER: US/09/773,877B		
; CURRENT FILING DATE: 2001-01-31		
; NUMBER OF SEQ ID NOS: 27		
; SOFTWARE: PatentIn version 3.0		
; SEQ ID NO 13		
; LENGTH: 1674		
; TYPE: DNA		
; ORGANISM: Artificial Sequence		
; FEATURE:		
; OTHER INFORMATION: Flt1(1-3 deltaB) (Mut 1)		
; NAME/KEY: CDS		
; LOCATION: (1)..(1674)		
US-09-773-877B-13		
Query Match		71.7%; Score 987.4; DB 4; Length 1674;
Best Local Similarity		86.1%; Pred. No. 2.6e-254;
Matches 1119; Conservative		0; Mismatches 171; Indels 9; Gaps 2;
QY	79	AGTGATACCGGTAGACCTTTTCGTAGAGATGTACAGTGAATCCCGAAATATATACATG 138

385	Db	 AGTGATACAGGTAGACCTTTTCGTAGAGATGTACAGTGAAATCCCCGAAATTTATACACATG	444
139	Qy	 ACTGAAGGAAGGGAGCTCGTCATTCCCTCGCGGGTTACGTACCTAACATCACTGTTACT	198
445	Db	 ACTGAAGGAAGGGAGCTCGTCATTCCCTCGCGGGTTACGTACCTAACATCACTGTTACT	504
199	Qy	 TTAAAAAGTTTCCACTTTGACACTTTTGATCCCTGATGGAACCGCATAACTCTGGGACAGT	258
505	Db	 TTAAAAAGTTTCCACTTTGACACTTTTGATCCCTGATGGAACCGCATAACTCTGGGACAGT	564
259	Qy	 AGAAAGGGCTTCATCATATCAAAATGCAGTAACAAAGAAATAGGGCTTCTGAACCTGTGAA	318
565	Db	 AGAAAGGGCTTCATCATATCAAAATGCAGTAACAAAGAAATAGGGCTTCTGAACCTGTGAA	624
319	Qy	 GCAACAGTCAATGGGCAATTGTATAAGCAACAACTATCTCACATTCACAAAACCAATACA	378
625	Db	 GCAACAGTCAATGGGCAATTGTATAAGCAACAACTATCTCACATTCACAAAACCAATACA	684
379	Qy	 ATCATAGATGTGGTTCCTGAGTCCGCTCATCGAAATTGAACTATCTGTTGGAGAAAAGCTT	438
685	Db	 ATCATAGATGTCCAAATAAGACACACAGCCGAGTCAAAATTACTTAGAGGCCATACTCTT	744
439	Qy	 GTCCTTAAATTGTACAGCAAGAACTGAACATAAATGTGGGATGTGACTTCAACTGGGAATAC	498
745	Db	 GTCCTCAATTGTACTGCTACCACTCCCTTGAAACACGAGAGTTCAATGACTCGGAGTTAC	804
499	Qy	 CCTTCTTCGAAGCATCAGCATAGAAACTTGTAAACCGAGACCTTAAAAACCCAGTCTGGG	558
805	Db	 CCTGATGAAATTGACCAAGCAATTCCTCATGCCCAACATATTCTACAGTGTCTTACTATT	864
559	Qy	 AGTGAGATGAAGAAATTTTGGACACCTTAACTATAGATGTGTGTAACCCGGAGTGACAA	618
865	Db	 GACAAATGCAGAACAAAGCAAAAGGACTTTATACTTGTGCTGTAA---GGAGTGGACCA	921
619	Qy	 GGATTGTACACTGTGCGAGCATCCAGTGGGCTGATGACCAAGAAGAACAGCATTTGTCTC	678
922	Db	 TCATTCAAACTGTGTAACACCTC-----AGTGCATATATATGATAAGCAGGCCCGGGC	975
679	Qy	 AGGTCCTAGAAAGGACAAACTCACACATGCCACCGTGCCAGCACCTGACTGACTCTTG	738
976	Db	 GAGCCCAAACTTTGTGACAAAACTCACATGCCCCACCTGTCGCCAGCACCTGAACTCCTG	1035
739	Qy	 GGGGGACCGTCAGTCTTCTCTTCCCCCCCCAAAGCCCAAGACACCCCTCATGATCTCCCGG	798
1036	Db	 GGGGGACCGTCAGTCTTCTCTTCCCCCCCCAAAGCCCAAGACACCCCTCATGATCTCCCGG	1095
799	Qy	 ACCCCTGAGGTCAATCGTGGTGGAGCGTGAAGCCACGAAGACCTCGAGGTCAAGTTC	858
1096	Db	 ACCCCTGAGGTCAATCGTGGTGGAGCGTGAAGCCACGAAGACCTCGAGGTCAAGTTC	1155
859	Qy	 AATGTGTACGTGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCCGGAGGAGCAG	918
1156	Db	 AATGTGTACGTGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCCGGAGGAGCAG	1215
919	Qy	 TACAAACAGCAGTACCGTGTGGTTCAGCGTCTCTACCCGTCTGCAACACAGGACTGCTCAAT	978
1216	Db	 TACAAACAGCAGTACCGTGTGGTTCAGCGTCTCTACCCGTCTGCAACACAGGACTGCTCAAT	1275
979	Qy	 GGCAAGGAGTCAAGTGTCAAGGTTCTCCAAACAAAGCCCTCCAGCGCCCATCGAGAAACC	1038
1276	Db	 GGCAAGGAGTCAAGTGTCAAGGTTCTCCAAACAAAGCCCTCCAGCGCCCATCGAGAAACC	1335
1039	Qy	 ATCTCCAAAGCCAAAGGGCAGCCCGAGAACCAAGGTGTACACCTTGCCCCCATCCCGG	1098
1336	Db	 ATCTCCAAAGCCAAAGGGCAGCCCGAGAACCAAGGTGTACACCTTGCCCCCATCCCGG	1395
1099	Qy	 GATGAGCTGACCAAGAACCAAGGTGAGCTGAGCTGCTGCTGGTCAAGAGCTTCTATCCAGC	1158
1396	Db	 GATGAGCTGACCAAGAACCAAGGTGAGCTGAGCTGCTGCTGGTCAAGAGCTTCTATCCAGC	1455
1159	Qy	 GACATCCCGGTGGAGTGGGAGCAATGGCGCGCGAGAACCAACTACAAGACCAACGCTT	1218

Db	1456	GACATGCCCGTGGAGTGGGAGAGCAATGGGACCGGAGAACAACTATCAAGACCAACGCCT	1515
Qy	1219	CCCGTGTGGACTCCGACGGCTCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGC	1278
Db	1516	CCCGTGTGACTCCGACGGCTCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGC	1575
Qy	1279	AGTGGCAGCAGGGGAAACGTCTTCTCTCATGCTCCGTGATGATGAGGCTCTGCACAACCAC	1338
Db	1576	AGTGGCAGCAGGGGAAACGTCTTCTCTCATGCTCCGTGATGATGAGGCTCTGCACAACCAC	1635
Qy	1339	TACAGCAGAGAGCCCTCTCCCTGTCTCCGGGTAAATGA	1377
Db	1636	TACAGCAGAGAGCCCTCTCCCTGTCTCCGGGTAAATGA	1674
RESULT 7			
US-09-773-877B-19			
; Sequence 19, Application US/09773877B			
; Patent No. 6833349			
; GENERAL INFORMATION:			
; APPLICANT: Xia, Yu-Ping et al.			
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES			
; FILE REFERENCE: REG 710b			
; CURRENT APPLICATION NUMBER: US/09/773,877B			
; CURRENT FILING DATE: 2001-01-31			
; NUMBER OF SEQ ID NOS: 27			
; SOFTWARE: PatentIn version 3.0			
; SEQ ID NO 19			
; LENGTH: 1704			
; TYPE: DNA			
; ORGANISM: Artificial Sequence			
; FEATURE:			
; OTHER INFORMATION: Fltl(1-3 R->N) (Mut 4)			
; NAME/KEY: CDS			
; LOCATION: (1)..(1704)			
US-09-773-877B-19			
Query Match 71.3%; Score 982.4; DB 4; Length 1704;			
Best Local Similarity 85.4%; Pred. No. 5.7e-253;			
Matches 1132; Conservative 0; Mismatches 161; Indels 33; Gaps 2;			
Qy	79	AGTGATACCGGTAGACCTTTTCGTAGAGATGTCACAGTGAAATCCCGGAAATTATACACATG	138
Db	385	AGTGATACAGGTAGACCTTTTCGTAGAGATGTCACAGTGAAATCCCGGAAATTATACACATG	444
Qy	139	ACTGAAGGAAGGAGCTCGTCATTCCCTCGCGGGTTACGTCACCTAACATCACTGTTTACT	198
Db	445	ACTGAAGGAAGGAGCTCGTCATTCCCTCGCGGGTTACGTCACCTAACATCACTGTTTACT	504
Qy	199	TTAAAAAGTTTTCATTGTGACATTTTGATCCCTGTAGTGAAGAAACGATATCTGGGACAGT	258
Db	505	TTAAAAAGTTTTCACATTGTGACATTTTGATCCCTGTAGTGAAGAAACGATATCTGGGACAGT	564
Qy	259	AGAAAGGCTTCATCATATCAAAATGCAACGTACAAAGAAATAGGGCTTCTGACCTGTGAA	318
Db	565	AGAAAGGCTTCATCATATCAAAATGCAACGTACAAAGAAATAGGGCTTCTGACCTGTGAA	624
Qy	319	GCAACAGTCAATGGGCAATTTGTATAGACAAAACCTATCTCACATCGACAAAACCAATACA	378
Db	625	GCAACAGTCAATGGGCAATTTGTATAGACAAAACCTATCTCACATCGACAAAACCAATACA	684
Qy	379	ATCATAGATGTGTTCTGAGTCCGTCTCATGGAAATTGAACATATCTGTTGAGAAAAGCTTT	438
Db	685	ATCATAGATGTCCAAATTAAGACACACCGCCAGTCAAAATTTACTTAGAGGCCATACCTCTT	744
Qy	439	GTCTTAATTTGTACAGCAAGAACTGAACTAAATGTGGGGATTCACITTCAACTGGGAATAC	498
Db	745	GTCTTAATTTGTACTGTCTACCACTCCCTTGAACAGAGTTCAATGACCTGGAGTTAC	804
Qy	499	CTTCTTCGAAGCATACAGCATAGAAACTTTGTAAACCGAGACCTTAAAAACCCAGTCTGGG	558
Db	805	CTCATGAAAAAATAAGACCGCTTCGTGAAGGCGACGAAATTGACCAAGCAATTC----	860

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Qy 559 AGTGAGATGAAGAAATTTTGGACACCTTAACCTATATAGATGGTGTAAACCCGAGGTGACCAA 618
Db 861 --CCATGCCAACATATCTACAGGTCTTCTACTATTGACAAATCGAGAAACAAAGACAAA 918
Qy 619 GGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAGAGACACACATTGTGTC 678
Db 919 GGACTTTATACTTGTGTGTAAGAGAGTGGACCATCATTTCAAAATCTGTAAACACCTCAGTG 978
Qy 679 AGGGTCCATGAAA-----GGACAAAACCTCACACATGC 711
Db 979 CATATATATGATAAAGCAGCGCCGGGAGAGCCCAATCTTGTGACAAAACCTCACACATGC 1038
Qy 712 CCACCGTGCCAGACCTGAACCTCTTGGGGGAGCCGTCAGTCTTCTCTTCCCGCCCAAAA 771
Db 1039 CCACCGTGCCAGACCTGAACCTCTTGGGGGAGCCGTCAGTCTTCTCTTCCCGCCCAAAA 1098
Qy 772 CCCAAGGACACCTCATGATCTCCCGACCCCTGAGGTACATGCTCGTGGTGGAGCTG 831
Db 1099 CCCAAGGACACCTCATGATCTCCCGACCCCTGAGGTACATGCTCGTGGTGGAGCTG 1158
Qy 832 AGCCACGAAGACCTCTGAGGTCAAGTTCAACTGGTACGTCGACGCGGTGGAGGTGCATAAT 891
Db 1159 AGCCACGAAGACCTCTGAGGTCAAGTTCAACTGGTACGTCGACGCGGTGGAGGTGCATAAT 1218
Qy 892 GCCAAGACAAAGCCGGGAGGAGCAGTACAAACAGCACGTACCGTGTGTCAGCGTCTC 951
Db 1219 GCCAAGACAAAGCCGGGAGGAGCAGTACAAACAGCACGTACCGTGTGTCAGCGTCTC 1278
Qy 952 ACCGTCTGCACAGNCTGGCTGAATGGCAAGAGGTACAAGTGCAGAGTCTCCACAAA 1011
Db 1279 ACCGTCTGCACAGNCTGGCTGAATGGCAAGAGGTACAAGTGCAGAGTCTCCACAAA 1338
Qy 1012 GCCTTCCAGCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCGCAGAACCA 1071
Db 1339 GCCTTCCAGCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCGCAGAACCA 1398
Qy 1072 CAGGTGTACACCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCCAGTGCAGCTGACC 1131
Db 1399 CAGGTGTACACCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCCAGTGCAGCTGACC 1458
Qy 1132 TGCTGTGTAAGGCTTCTATCCAGCGCATCGCCGTGGAGTGGAGAGCAATGGGCAG 1191
Db 1459 TGCTGTGTAAGGCTTCTATCCAGCGCATCGCCGTGGAGTGGAGAGCAATGGGCAG 1518
Qy 1192 CCGGAGAACACTACAGACCCAGCTCCGCTGCTGAGCTCCGACGCTCTCTTCTTCCCTC 1251
Db 1519 CCGGAGAACACTACAGACCCAGCTCCGCTGCTGAGCTCCGACGCTCTCTTCTTCCCTC 1578
Qy 1252 TACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACTCTTCTCATGCTCC 1311
Db 1579 TACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACTCTTCTCATGCTCC 1638
Qy 1312 GTGATGATGAGGCTCTGCAACCACTACACGAGAAAGCCTCTCCCTGTCTCCGGGT 1371
Db 1639 GTGATGATGAGGCTCTGCAACCACTACACGAGAAAGCCTCTCCCTGTCTCCGGGT 1698
Qy 1372 AAATGA 1377
Db 1699 AAATGA 1704
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## RESULT 8

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US-09-773-877B-11
; Sequence 11, Application US/09773877B
; Patent No. 683349
; GENERAL INFORMATION:
; APPLICANT: Xia, Yu-Ping et al.
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
; FILE REFERENCE: REG 710b
; CURRENT APPLICATION NUMBER: US/09/773,877B
; CURRENT FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin version 3.0
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; SEQ ID NO 11
; LENGTH: 1704
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Flt1(1-3)-Fc
; NAME/KEY: CDS
; LOCATION: (1)..(1704)
US-09-773-877B-11
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Query Match 71.2%; Score 980.8; DB 4; Length 1704;
Best Local Similarity 85.3%; Pred. No. 1.5e-252;
Matches 1131; Conservative 0; Mismatches 162; Indels 33; Gaps 2;
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Qy 79 AGTGATACCGGTAGACCTTTTCGTAGAGATGTACAGTGAATCCCGGAAATATATACATG 138
Db 385 AGTGATACAGGTAGACCTTTTCGTAGAGATGTACAGTGAATCCCGGAAATATATACATG 444
Qy 139 ACTGAAGGAAGGAGGTCTGTCATTCCTGCGGGTTACGTCACTAACATCACTGTTACT 198
Db 445 ACTGAAGGAAGGAGGTCTGTCATTCCTGCGGGTTACGTCACTAACATCACTGTTACT 504
Qy 199 TTAATAAAGTTTCCACTTGCACCTTTGATCCCTGATGGAAGGCGCATAACTCGGACAGT 258
Db 505 TTAATAAAGTTTCCACTTGCACCTTTGATCCCTGATGGAAGGCGCATAACTCGGACAGT 564
Qy 259 AGAAAGGGCTTCATCATATCAAAATGCAACGTACAAAGAAATAGGGCTTCTGACCTGAA 318
Db 565 AGAAAGGGCTTCATCATATCAAAATGCAACGTACAAAGAAATAGGGCTTCTGACCTGAA 624
Qy 319 GCAACAGTCAATGGGCAATTGTATAAGACAAATCTCTCAATCGACAAACCAATACA 378
Db 625 GCAACAGTCAATGGGCAATTGTATAAGACAAATCTCTCAATCGACAAACCAATACA 684
Qy 379 ATCATAGATGTGTTCTGAGTCCGTCTCATGGAATGAACATATCTGTTGGAGAAAGCTT 438
Db 685 ATCATAGATGTGTTCAAAATGAAGCACACCGCCAGTCAAAATTAATTAGAGCCCATCTCT 744
Qy 439 GTCTTAAATTTGACAGCAAGAACTGAACTAAATGTGGGATTCGATTTCAACTCGGAATAC 498
Db 745 GTCTCAATTTGATCTGCTACCACTCCCTTGAACACGAGAGTTCAATGACTGGAGTTAC 804
Qy 499 CTTTCTTTCGAAGCATCAGCATAAAGAACTTTGTAACCCGAGACCTTAAACCCAGTCTGGG 558
Db 805 CCT-----GATGAAAAAATAAGAGAGCTTCCGTAAGGCGACGAATTTGACCAAGCAAT 858
Qy 559 AGTGAGATGAAGAAATTTTGGACACCTTAACTATAGATGGTGTAAACCCGAGGTGACAA 618
Db 859 TCCCATGCCAACATATTCTACAGTGTCTTACTATTGACAAAAATGCAGAAACAAAGACAA 918
Qy 619 GGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAGAGAACACACATTTGTC 678
Db 919 GGACTTTATCTTGTCTGTTAAGGAGTGGACCATCATTAATCTGTTAAACCTCACTAGTG 978
Qy 679 AGGGTCCATGAAA-----GGACAAAACCTCACACATGC 711
Db 979 CATATATATGATAAAGCAGCGCCGGGAGAGCCCAATCTTGTGACAAAACCTCACACATGC 1038
Qy 712 CCACCGTGCCAGACCTGAACCTCTTGGGGGAGCCGTCAGTCTCTCTTCTTCCCGCCCAAAA 771
Db 1039 CCACCGTGCCAGACCTGAACCTCTTGGGGGAGCCGTCAGTCTCTCTTCTTCCCGCCCAAAA 1098
Qy 772 CCCAAGGACACCTCATGATCTCCCGACCCCTGAGGTACATGCTCGTGGTGGAGCTG 831
Db 1099 CCCAAGGACACCTCATGATCTCCCGACCCCTGAGGTACATGCTCGTGGTGGAGCTG 1158
Qy 832 AGCCACGAAGACCTCTGAGGTCAAGTTCAACTGGTACGTCGACGCGGTGGAGGTGCATAAT 891
Db 1159 AGCCACGAAGACCTCTGAGGTCAAGTTCAACTGGTACGTCGACGCGGTGGAGGTGCATAAT 1218
Qy 892 GCCAAGACAAAGCCGGGAGGAGCAGTACAAACAGCACGTACCGTGTGTCAGCGTCTC 951
Db 1219 GCCAAGACAAAGCCGGGAGGAGCAGTACAAACAGCACGTACCGTGTGTCAGCGTCTC 1278
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QY 952 ACGTCTCTGCACGAGGACTGGCTGAATGGCAAGAGTACAAAGTGCAGGTCTTCAACAA 1011
Db |||||
QY 1279 ACGTCTCTGCACGAGGACTGGCTGAATGGCAAGAGTACAAAGTGCAGGTCTTCAACAA 1338
Db |||||
QY 1012 GCCTCCCGAGCCCGCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGAACCA 1071
Db |||||
QY 1339 GCCTCCCGAGCCCGCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGAACCA 1398
Db |||||
QY 1072 CAGGTGTACACCTGCCCCCATCCCGGATGAGTGCACCAAGAACAGGTGACCTGACC 1131
Db |||||
QY 1399 CAGGTGTACACCTGCCCCCATCCCGGATGAGTGCACCAAGAACAGGTGACCTGACC 1458
Db |||||
QY 1132 TGCTGTGTCAAAGGCTTCTATCCAGCGACATCCCGTGGAGTGGAGGAGCAATGGGAG 1191
Db |||||
QY 1459 TGCTGTGTCAAAGGCTTCTATCCAGCGACATCCCGTGGAGTGGAGGAGCAATGGGAG 1518
Db |||||
QY 1192 CCGGAGAACAACTACAGAACCGCCCTCCCGTGTGAGTCTCCGACGGCTCTTCTTCCCTC 1251
Db |||||
QY 1519 CCGGAGAACAACTACAGAACCGCCCTCCCGTGTGAGTCTCCGACGGCTCTTCTTCCCTC 1578
Db |||||
QY 1252 TACAGCAAGCTTACCGTGGACAGAGAGGTGGCAGAGGGGAAAGTCTTCTCATGCTCC 1311
Db |||||
QY 1579 TACAGCAAGCTTACCGTGGACAGAGAGGTGGCAGAGGGGAAAGTCTTCTCATGCTCC 1638
Db |||||
QY 1312 GTGATGCATGAGGCTCTGCACAACTACTACACGACAGAGGCTCTCCCTGTCTCCGGGT 1371
Db |||||
QY 1639 GTGATGCATGAGGCTCTGCACAACTACTACACGACAGAGGCTCTCCCTGTCTCCGGGT 1698
Db |||||
QY 1372 AAATGA 1377
Db |||||
QY 1699 AAATGA 1704
Db |||||
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## RESULT 9

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US-08-227-496C-14
; Sequence 14, Application US/08227496C
; Patent No. 6130202
; GENERAL INFORMATION:
; APPLICANT: Greve, Jeffrey M.
; APPLICANT: McClelland, Alan
; TITLE OF INVENTION: Multimeric Forms of Human
; TITLE OF INVENTION: Rhinovirus Receptor Protein
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bayer Corporation
; STREET: 400 Morgan Lane
; CITY: West Haven
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06516
; COMPUTER READABLE FORM:
; MEDIUM TYPE: diskette, 1.44 Mb storage
; COMPUTER: Dell Optiplex GX1
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect 8.0 for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/227,496C
; FILING DATE: 04/14/94
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/903,069
; FILING DATE: 06/22/92
; APPLICATION NUMBER: 07/704,984
; FILING DATE: 05/24/91
; APPLICATION NUMBER: 07/556,238
; FILING DATE: 07/20/90
; ATTORNEY/AGENT INFORMATION:
; NAME: Barbara A. Shimei
; REGISTRATION NUMBER: 29,862
; REFERENCE/DOCKET NUMBER: MTI 214.2C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203) 812-2786
```

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; TELEFAX: (203) 812-5492
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2043 bp
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FEATURE:
; NAME/KEY: t1CAM(453)/IgG fusion
; OTHER INFORMATION: bp 1-1359 = nucleotides coding
; OTHER INFORMATION: for amino acid residues 1-453 of ICAM-1; bp 1360-
; OTHER INFORMATION: 2040 = nucleotides coding for amino acid residues
; OTHER INFORMATION: 216-442 of human heavy chain IgG1; bp 2401-2043 =
; OTHER INFORMATION: stop codon
; US-08-227-496C-14
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Query Match 49.8%; Score 686; DB 3; Length 2043;
Best Local Similarity 95.9%; Pred. No. 1.6e-173;
Matches 704; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
QY 644 GTGGGTGTGATGACCAAGAAAGACAGCACATTTGTTCAGGGTCCATGAAAGGACAAACTC 703
Db |||||
QY 1310 GGGAGGTACCCCGCAAGGTGACCGTGAATGTGCTCTCCCCCGGTATGAGGACAAACTC 1369
Db |||||
QY 704 ACACATGCCACCGTCCCGCAGCACCTGAACTCTCTGGGGGAGCCGTGAGTCTTCTCTTCC 763
Db |||||
QY 1370 ACACATGCCACCGTCCCGCAGCACCTGAACTCTCTGGGGGAGCCGTGAGTCTTCTCTTCC 1429
Db |||||
QY 764 CCCCACCAACCAAGGACACCCCTCATGATCTCCGGACCCCTGAGGTCACTGCGTGGTGG 823
Db |||||
QY 1430 CCCCACCAACCAAGGACACCCCTCATGATCTCCGGACCCCTGAGGTCACTGCGTGGTGG 1489
Db |||||
QY 824 TGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGG 883
Db |||||
QY 1490 TGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGG 1549
Db |||||
QY 884 TGCATAATGCCAAGACAAAGCCCGGGAGGAGCAGTACAAACAGCAGTACCGTGTGGTCA 943
Db |||||
QY 1550 TGCATAATGCCAAGACAAAGCCCGGGAGGAGCAGTACAAACAGCAGTACCGGTTGGTCA 1609
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QY 944 GCGTCTCACCGTCTGTGCACAGGAGTGTGCTGAATGGGAGGAGTACAAAGTCAAGGTCT 1003
Db |||||
QY 1610 GCGTCTCACCGTCTGTGCACAGGAGTGTGCTGAATGGGAGGAGTACAAAGTCAAGGTCT 1669
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QY 1004 CCAACAAAGCCCTCCCGAGCCCGCCCATCGAGAAACCATCTCCAAAGCCAAAGGACGCCCC 1063
Db |||||
QY 1670 CCAACAAAGCCCTCCCGAGCCCGCCCATCGAGAAACCATCTCCAAAGCCAAAGGACGCCCC 1729
Db |||||
QY 1064 GAGAACCCAGGTGTACACCTTGCCCGCCATCCCGGATGAGTGCACCAAGAACCAAGTCA 1123
Db |||||
QY 1730 GAGAACCCAGGTGTACACCTTGCCCGCCATCCCGGATGAGTGCACCAAGAACCAAGTCA 1789
Db |||||
QY 1124 GCCTGACCTGCTGTCAAAGGCTTCTATCCAGCGACATCCCGCTGGAGTGGGAGAGCA 1183
Db |||||
QY 1790 GCCTGACCTGCTGTCAAAGGCTTCTATCCAGCGACATCCCGCTGGAGTGGGAGAGCA 1849
Db |||||
QY 1184 ATGGGCGAGCCGGAGAACAACTACAAAGCCACCGCTCCCGTGTGGACTCCGACGGTCTCT 1243
Db |||||
QY 1850 ATGGGCGAGCCGGAGAACAACTACAAAGCCACCGCTCCCGTGTGGACTCCGACGGTCTCT 1909
Db |||||
QY 1244 TCTTCTCTTACAGCAAGGTTCACCGTGGACAGAGCAGGTGGCAGCAGGGGAAAGTCTTCT 1303
Db |||||
QY 1910 TCTTCTCTTACAGCAAGGTTCACCGTGGACAGAGCAGGTGGCAGCAGGGGAAAGTCTTCT 1969
Db |||||
QY 1304 CATGCTCCGTGATGATGAGGCTCTGCAACCACTACAGCAGAGAGACCTCTCCCTGT 1363
Db |||||
QY 1970 CATGCTCCGTGATGATGAGGCTCTGCAACCACTACAGCAGAGAGACCTCTCCCTGT 2029
Db |||||
QY 1364 CTCCGGGTAAATGA 1377
Db |||||
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[illegible][illegible]



Query Match	49.7%	Score 684	DB 3	Length 1182
Best Local Similarity	100.0%	Pred. No. 4.2e-173		
Matches 684	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	694	GACAAACTCACACATGCCACCGTGGCCAGACACCTGAACTCCTGGGGGACCGTCAGTC	753	
DB	483	GACAAACTCACACATGCCACCGTGGCCAGACACCTGAACTCCTGGGGGACCGTCAGTC	542	
QY	754	TTCTCTTCCCCCAAAACCCCAAGGACACCCCTCATGATCTCCCGGACCCCTTGAGGTCACA	813	
DB	543	TTCTCTTCCCCCAAAACCCCAAGGACACCCCTCATGATCTCCCGGACCCCTTGAGGTCACA	602	
QY	814	TGCGTGGTGGTGGACGTGAGCCACGAAAGACCCCTGAGGTCAAGTTCAACTGTGACGTGAC	873	
DB	603	TGCGTGGTGGTGGACGTGAGCCACGAAAGACCCCTGAGGTCAAGTTCAACTGTGACGTGAC	662	
QY	874	GGCGTGGAGGTGCATAATGCGCAAGACAAAGCCGCGGAGGAGCAGTACAAACAGCACGTAC	933	
DB	663	GGCGTGGAGGTGCATAATGCGCAAGACAAAGCCGCGGAGGAGCAGTACAAACAGCACGTAC	722	
QY	934	CGTGTGGTCAAGGTCTCTACCGTCTTGACACGAGACTGGCTGAATGGCAAGGAGTACAAAG	993	
DB	723	CGTGTGGTCAAGGTCTCTACCGTCTTGACACGAGACTGGCTGAATGGCAAGGAGTACAAAG	782	
QY	994	TGCAAGGTCTCCAAACAAAGCCCTCCAGCCCCCATCGAAACCAACCATCTCCAAAGCCAAA	1053	
DB	783	TGCAAGGTCTCCAAACAAAGCCCTCCAGCCCCCATCGAAACCAACCATCTCCAAAGCCAAA	842	
QY	1054	GGCGACCCCGAGAACCAACAGGTGTACACCTGCCGCCCATCCCGGGATGAGCTGACCAAG	1113	
DB	843	GGCGACCCCGAGAACCAACAGGTGTACACCTGCCGCCCATCCCGGGATGAGCTGACCAAG	902	
QY	1114	AACAGGTCAAGGTCAAGTGGCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAG	1173	
DB	903	AACAGGTCAAGGTCAAGTGGCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAG	962	
QY	1174	TGGGAGCAANTGGGCGAGCCGAGAACACTACAGACCAACCGCTCCCGTGTGACTGCC	1233	
DB	963	TGGGAGCAANTGGGCGAGCCGAGAACACTACAGACCAACCGCTCCCGTGTGACTGCC	1022	
QY	1234	GACGGTCTCTTCTCTACAGCAAGCTCACCGTGGCAAGAGCAGGTGGCAGCAGGGG	1293	
DB	1023	GACGGTCTCTTCTCTACAGCAAGCTCACCGTGGCAAGAGCAGGTGGCAGCAGGGG	1082	
QY	1294	AAGCTTCTCATGTCTCGTGTGATGATGAGGTCTTGCAACCACTACCGCAGAAGAGC	1353	
DB	1083	AAGCTTCTCATGTCTCGTGTGATGATGAGGTCTTGCAACCACTACCGCAGAAGAGC	1142	
QY	1354	CTCTCCCTGTCTCCGGGTAAATGA	1377	
DB	1143	CTCTCCCTGTCTCCGGGTAAATGA	1166	
RESULT 14				
US-08-488-376-19				
; Sequence 19, Application US/08488376				
; Patent No. 581524				
; GENERAL INFORMATION:				
; APPLICANT: BRAMS, Peter				
; APPLICANT: CHAMAT, Soulaime Salim				
; APPLICANT: PAN, Li-Zhen				
; APPLICANT: WALSH, Edward E.				
; APPLICANT: HEARD, Cheryl Janne				
; APPLICANT: NEWMAN, Roland Anthony				
; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN				
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND				
; TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF				
; NUMBER OF SEQUENCES: 19				
; CORRESPONDENCE ADDRESS:				
; ADDRESSEE: Burns, Doane, Swecker & Mathis				
; STREET: P.O. Box 1404				
; CITY: Alexandria				

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Db      1285 GACGGCTCTTCTTCTCTACGAAGCTCACCGTGACAAAGCTCACCGTGACAGGCTGGCAGCAGGGG 1344
Qy      1294 AACGTCTTCTCATGCTCCGCTGATGCGATGAGGCTCTGCACAAACCACTACACGACGAAGAGC 1353
Db      1345 AACGTCTTCTCATGCTCCGCTGATGCGATGAGGCTCTGCACAAACCACTACACGACGAAGAGC 1404
Qy      1354 CTCTCCCTGTCTCCGGGTAAATGA 1377
Db      1405 CTCTCCCTGTCTCCGGGTAAATGA 1428

RESULT 15
US-08-634-223-19
; Sequence 19, Application US/08634223
; Patent No. 5840298
; GENERAL INFORMATION:
; APPLICANT: BRAMS, Peter
; APPLICANT: CHAMAT, Soulaïma Salim
; APPLICANT: PAN, Li-Zhen
; APPLICANT: WALSH, Edward E.
; APPLICANT: HEARD, Roland Anthony
; APPLICANT: NEWMAN, Roland Anthony
; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
; TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/634,223
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,376
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-150
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1428 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1428
; US-08-634-223-19

Query Match 49.7%; Score 684; DB 2; Length 1428;
Best Local Similarity 100.0%; Pred. No. 4.6e-173;
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      694 GACAAACTCACACATGCCCGTGGCCAGACCTGAACTCTCTGGGGGACCGTCAGTC 753
Db      745 GACAAAACTCACACATGCCCGTGGCCAGCACCTGAACTCTCTGGGGGACCGTCAGTC 804
Qy      754 TTCTCTTCTCCCGGACCAAGGACACACCTCATGATCTCCCGGACCCCTGAGGTGACA 813
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Db      805 TTCTCTTCTCCCGGACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTGACA 864
Qy      814 TCGTGTGGTGGGACGTGAGCCACGAAGACCTTGAGGTCAAGTTCAACTGGTACGTGGAC 873
Db      865 TCGTGTGGTGGGACGTGAGCCACGAAGACCTTGAGGTCAAGTTCAACTGGTACGTGGAC 924
Qy      874 GCGGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAAACAGCAGCTAC 933
Db      925 GCGGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAAACAGCAGCTAC 984
Qy      934 CGTGTGGTCAGCGTCTCTCACCGTCTGCACACGAGTCTGGCTCAATGGCAAGAGGTACAAAG 993
Db      985 CGTGTGGTCAGCGTCTCTCACCGTCTGCACACGAGTCTGGCTCAATGGCAAGAGGTACAAAG 1044
Qy      994 TCGAAGGTCTCCAAACAAAGCCCTCCAGCCCGCCATCGAGAAAACCACTCTCCAAAGCCAAA 1053
Db      1045 TCGAAGGTCTCCAAACAAAGCCCTCCAGCCCGCCATCGAGAAAACCACTCTCCAAAGCCAAA 1104
Qy      1054 GGGCAGCCCGAGAACACAGGTGTACACCCCTGCCATCCCGGGATGAGCTGACCAAG 1113
Db      1105 GGGCAGCCCGGAGAACACAGGTGTACACCCCTGCCATCCCGGGATGAGCTGACCAAG 1164
Qy      1114 AACCCAGGTCTGAGCTGACCTGCTGCTCAAGGCTTCTATCCAGCGACATCGCCCGTGGAG 1173
Db      1165 AACCCAGGTCTGAGCTGACCTGCTGCTCAAGGCTTCTATCCAGCGACATCGCCCGTGGAG 1224
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Qy      1234 GACGGCTCTTCTTCTCTTACAGCAAGCTCACCGTGGACAAAGCAGGCTGGCAGCAGGGG 1293
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Db      1405 CTCTCCCTGTCTCCGGGTAAATGA 1428
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Search completed: September 23, 2005, 16:56:56

Job time : 275 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2005, 13:48:22 ; Search time 932 Seconds

(without alignments)  
9878.585 Million cell updates/sec

Title: US-10-811-170-1

Perfect score: 1377

Sequence: 1 atggctcagctactgggacac.....ccctgtctccgggtaaatga 1377

Scoring table: IDENTITY NUC

Gapop 10\_0 , Gapext 1.0

Searched: 7400704 seqs, 3343079526 residues

Total number of hits satisfying chosen parameters: 14801408

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:\*

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- 19: /cgn2\_6/ptodata/2/pubpna/US10G\_PUBCOMB.seq:\*
- 20: /cgn2\_6/ptodata/2/pubpna/US10H\_PUBCOMB.seq:\*
- 21: /cgn2\_6/ptodata/2/pubpna/US10I\_PUBCOMB.seq:\*
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- 23: /cgn2\_6/ptodata/2/pubpna/US11A\_PUBCOMB.seq:\*
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- 26: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1377	100.0	1377	17	US-09-773-877A-25
2	1377	100.0	1377	10	US-10-609-775-9
3	1377	100.0	1377	20	US-10-860-958-1
4	1377	100.0	1377	21	US-10-830-902-1
5	1377	100.0	1377	21	US-10-897-802-1
6	1377	100.0	1377	21	US-10-880-021-9
7	1377	100.0	1377	21	US-10-909-011-3

8	1377	100.0	1377	22	US-10-988-243-15	Sequence 15, Appl
9	1377	100.0	1377	22	US-10-988-881-3	Sequence 3, Appl
10	1377	100.0	1377	24	US-11-016-097-15	Sequence 15, Appl
11	1377	100.0	1377	24	US-11-039-144-1	Sequence 1, Appl
12	1328.4	96.5	1453	10	US-09-773-877A-21	Sequence 21, Appl
13	1328.4	96.5	1453	17	US-10-609-775-7	Sequence 7, Appl
14	1328.4	96.5	1453	21	US-10-880-021-7	Sequence 7, Appl
15	1328.4	96.5	1453	21	US-10-909-011-1	Sequence 1, Appl
16	1328.4	96.5	1453	22	US-10-988-243-11	Sequence 11, Appl
17	1328.4	96.5	1453	22	US-10-988-881-1	Sequence 11, Appl
18	1328.4	96.5	1453	24	US-11-016-097-11	Sequence 11, Appl
19	1323.6	96.1	1377	21	US-10-855-559-12	Sequence 12, Appl
20	1049.2	76.2	1444	17	US-09-773-877A-23	Sequence 23, Appl
21	1049.2	76.2	1444	17	US-10-609-775-12	Sequence 12, Appl
22	1049.2	76.2	1444	21	US-10-880-021-12	Sequence 12, Appl
23	1049.2	76.2	1444	22	US-10-988-243-13	Sequence 13, Appl
24	1049.2	76.2	1444	24	US-11-016-097-13	Sequence 13, Appl
25	1039	75.5	1359	10	US-09-773-877A-15	Sequence 15, Appl
26	1039	75.5	1359	22	US-10-988-243-5	Sequence 5, Appl
27	1039	75.5	1359	24	US-11-016-097-5	Sequence 5, Appl
28	1032.4	75.0	1389	10	US-09-773-877A-17	Sequence 17, Appl
29	1032.4	75.0	1389	22	US-10-988-243-7	Sequence 7, Appl
30	1032.4	75.0	1389	24	US-11-016-097-7	Sequence 7, Appl
31	987.4	71.7	1674	10	US-09-773-877A-13	Sequence 13, Appl
32	987.4	71.7	1674	22	US-10-988-243-3	Sequence 3, Appl
33	987.4	71.7	1674	24	US-11-016-097-3	Sequence 3, Appl
34	982.4	71.3	1704	10	US-09-773-877A-19	Sequence 19, Appl
35	982.4	71.3	1704	22	US-10-988-243-9	Sequence 9, Appl
36	982.4	71.3	1704	24	US-11-016-097-9	Sequence 9, Appl
37	980.8	71.2	1704	10	US-09-773-877A-11	Sequence 11, Appl
38	980.8	71.2	1704	22	US-10-988-243-1	Sequence 1, Appl
39	980.8	71.2	1704	24	US-11-016-097-1	Sequence 1, Appl
40	687.8	49.9	1290	17	US-10-435-608-7	Sequence 7, Appl
41	687.8	49.9	1290	18	US-10-622-108-7	Sequence 7, Appl
42	687.8	49.9	1299	17	US-10-435-608-9	Sequence 9, Appl
43	687.8	49.9	1299	18	US-10-622-108-9	Sequence 9, Appl
44	687.2	49.9	1383	17	US-10-275-589-17	Sequence 17, Appl
45	687.2	49.9	1389	17	US-10-385-802-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1  
US-09-773-877A-25  
; Sequence 25, Application US/09773877A  
; Publication No. US2003001797A1  
; GENERAL INFORMATION:  
; APPLICANT: Xia, Yu-ping et al.  
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES  
; FILE REFERENCE: REG 710b  
; CURRENT APPLICATION NUMBER: US/09/773, 877A  
; CURRENT FILING DATE: 2001-01-31  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 25  
; LENGTH: 1377  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: VEGFR1R2.FcdeltaC1(a) Receptor  
; NAME/KEY: CDS  
; LOCATION: (1)..(1377)  
US-09-773-877A-25

Query Match 100.0%; Score 1377; DB 10; Length 1377;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGGTCAGCTACTGGGACACCGGGTCTGCTGTGGCGCTGCTCAGCTGTCTGCTTCTC 60  
DB 1 ATGGTCAGCTACTGGGACACCGGGTCTGCTGTGGCGCTGCTCAGCTGTCTGCTTCTC 60

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Db 121 CCCGAAATTTATACATGACTGAAGAAAGGGAGCTCGTCAATTCCTTCCGCGGTTCAGTCA 180
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QY 301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCAATTTGTATAGAACAATATCTCACA 360
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QY 361 CATCGACAACCAATACATCATAGATGGTTCGTAGTCCGCTCATGGAATTTGAACCTA 420
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QY 541 CTAATAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGGAGCACTTAACTATAGATGT 600
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QY 661 AAGAACAGCACATTTGTTCAGGGTCCATGAAAAGGACAAAACCTCACACATGCCCAACCGTGC 720
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RESULT 2
US-10-609-775-9
; Sequence 9, Application US/10609775
; Publication No. US20040014667A1
; GENERAL INFORMATION:
; APPLICANT: Thomas J. Daly
; APPLICANT: James P. Fandi
; APPLICANT: Nicholas J. Papadopoulos
; TITLE OF INVENTION: VSGF TRAPS AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: REG 7100
; CURRENT APPLICATION NUMBER: US/10/609,775
; PRIOR FILING DATE: 2003-06-30
; PRIOR APPLICATION NUMBER: 10/009,852
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/14142
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/138,133
; PRIOR FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1377
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-609-775-9

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	481	GACTTCAACTGGGAATACCCCTTCTTCGAAGCATCAGCATAGAACCTTGTTAAACCGGAGAC	540
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Qy	781	ACCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAA	840
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Qy	841	GACCTGAGGTCAAGTTCAACTGTGACGCGCGTGGAGTGCATATATGCCAAGACA	900
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Qy	901	AAGCCGGGAGGAGCAGTACACAGCACGTTACCGTGTGTCAGCGTCTCTACCGTCCGT	960
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Qy	1081	ACCTGCCCCCATCCCGGATGAGCTGACCAAGAACCAAGTTCAGCTGACCTGCTGCTGGTC	1140
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Db	1321	GAGGCTCTGCACAACCACTACACGACAGAGCCCTCTCCCTGTCTCCGGTAAATGA	1377

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: APPLICANT: Yamashiro, Darrell
: APPLICANT: Huang, Jianzhong
: APPLICANT: Yancopoulos, George
: APPLICANT: Rudge, John
: TITLE OF INVENTION: Method of Tumor Regression with VEGF
: TITLE OF INVENTION: Inhibitors
: FILE REFERENCE: REG 714A
: CURRENT APPLICATION NUMBER: US/10/860,958
: CURRENT FILING DATE: 2004-06-04
: PRIOR APPLICATION NUMBER: 60/476,425
: PRIOR FILING DATE: 2003-06-06
: NUMBER OF SEQ ID NOS: 2
: SOFTWARE: FastSEQ for Windows Version 4.0
: SEQ ID NO 1
: LENGTH: 1377
: TYPE: DNA
: ORGANISM: homo sapiens
: US-10-860-958-1

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Qy	61	ACAGGATCTAGTTCCGGAGTGATACCGGTAGACCTTTTCGTAGAGATGTACAGTGAATC 120			
Db	61	ACAGGATCTAGTTCCGGAGTGATACCGGTAGACCTTTTCGTAGAGATGTACAGTGAATC 120			
Qy	121	CCCGAAATTATACACATGACTGAAGGAAGGAGCTCGTCATTCCTGCCGGGTACGTCA 180			
Db	121	CCCGAAATTATACACATGACTGAAGGAAGGAGCTCGTCATTCCTGCCGGGTACGTCA 180			
Qy	181	CCTAAACATCACTGTTACTTTAAAAAGTTTCCACTTTGACACTTTGATCCCTGATGGAAAA 240			
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Qy	241	CGCATATCTGGGACAGTAGAAAGGCTTCATCATATCAAATCGAACAGTCAAGAAGAAATA 300			
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Qy	301	GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCAATTTGTATGAAGCAAACTATCTCACA 360			
Db	301	GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCAATTTGTATGAAGCAAACTATCTCACA 360			
Qy	361	CATCGCAAAACCAATACAAATCATAGATGTGGTCTCAGTCCGCTCATGGAATTGAACATA 420			
Db	361	CATCGCAAAACCAATACAAATCATAGATGTGGTCTCAGTCCGCTCATGGAATTGAACATA 420			
Qy	421	TCGTGTTGGAGAAAGCTGTCTTAAATGTTACAGCAAGAACTCAACTAAATGTGGGATTT 480			
Db	421	TCGTGTTGGAGAAAGCTGTCTTAAATGTTACAGCAAGAACTCAACTAAATGTGGGATTT 480			
Qy	481	GACTTCAACTGGGAATAACCCCTCTTCTGGAAGCATCAGCATAAAGAAACTTGTAAACCCGAGAC 540			
Db	481	GACTTCAACTGGGAATAACCCCTCTTCTGGAAGCATCAGCATAAAGAAACTTGTGTAAACCCGAGAC 540			
Qy	541	CTAAAAACCCAGTCTCGGAGTGAGATGAAGAAATTTTGTAGCAACCTTAACATAAGATGGT 600			
Db	541	CTAAAAACCCAGTCTCGGAGTGAGATGAAGAAATTTTGTAGCAACCTTAACATAAGATGGT 600			
Qy	601	GTAAACCGGAGTGACCAAGATTGTACCTGTGCAGCATCCAGTGGCTGATGACCAAG 660			
Db	601	GTAAACCGGAGTGACCAAGATTGTACCTGTGCAGCATCCAGTGGCTGATGACCAAG 660			
Qy	661	AAGAACAGCACATTTGTCAAGGTCCTATGAAGGACAAAACTCACACATGCCACCGTGC 720			
Db	661	AAGAACAGCACATTTGTCAAGGTCCTATGAAGGACAAAACTCACACATGCCACCGTGC 720			
Qy	721	CCAGCACCTGAACTCCTGGGGGACCGTCAAGTCTTCTCTTCCCCCAAAACCCCAAGGAC 780			

RESULT 3  
US-10-860-958-1  
; Sequence 1, Application US/10860958  
; Publication NO. US20040265309A1  
; GENERAL INFORMATION:  
; APPLICANT: Kandel, Jessica  
; APPLICANT: Holash, Jocelyn



Db	1141	AAAGGCTTCTATCCACCGGACATCGCCGTGGAGTGGGAGAGCAATGGGACGCCGGAGAAC	1200
Qy	1201	AACTACAAGACCAAGCCCTCCCGTCTGGAACTCCGACGGCTCCTTCTTCTCTACAGCAAG	1260
Db	1201	AACTACAAGACCAAGCCCTCCCGTCTGGAACTCCGACGGCTCCTTCTTCTCTACAGCAAG	1260
Qy	1261	CTCACCGTGACAAGAGACAGGTGGCAGCAGGGGAAAGCTTCTCATGCTCCGTGATGCAT	1320
Db	1261	CTCACCGTGACAAGAGACAGGTGGCAGCAGGGGAAAGCTTCTCATGCTCCGTGATGCAT	1320
Qy	1321	GAGGCTCTGCAACAACACTACACGAGAAGAGCCCTTCCCTGTCTCCGGGTAATATGA	1377
Db	1321	GAGGCTCTGCAACAACACTACACGAGAAGAGCCCTTCCCTGTCTCCGGGTAATATGA	1377

## RESULT 5

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US-10-897-802-1
; Sequence 1, Application US/10897802
; Publication No. US2005032699A1
; GENERAL INFORMATION:
; APPLICANT: Jocelyn Holash
; APPLICANT: Robert Jaffe
; APPLICANT: Limin Hu
; APPLICANT: George D. Yancopoulos
; TITLE OF INVENTION: Composition of a VEGF Antagonist and an Anti-Proliferative Agent
; FILE REFERENCE: REG 715B
; CURRENT APPLICATION NUMBER: US/10/897,802
; CURRENT FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: 60/493,971
; PRIOR FILING DATE: 2003-08-08
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1377
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-897-802-1

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Query Match	100.0%	Score 1377;	DB 21;	Length 1377;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1377;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	ATGGTCAGCTACTGGGACACCGGGGTCTGCTGTGCGCGCTGCTCAGCTGTCTCGTTC	60	
Db	1	ATGGTCAGCTACTGGGACACCGGGGTCTGCTGTGCGCGCTGCTCAGCTGTCTCGTTC	60	
Qy	61	ACAGGATCTAGTTCCCGGAAGTGATACCGGTAGACCTTTGCTGAGAGATGTTACAGTGAATC	120	
Db	61	ACAGGATCTAGTTCCCGGAAGTGATACCGGTAGACCTTTGCTGAGAGATGTTACAGTGAATC	120	
Qy	121	CCGGAATTATACACATGACTGAAGGAGGAGCTCGTCACTTCCTGCGGGTTACGTCA	180	
Db	121	CCGGAATTATACACATGACTGAAGGAGGAGCTCGTCACTTCCTGCGGGTTACGTCA	180	
Qy	181	CCTAACATCACTGTTCATTTTAAAAAGTTTCCACTTGACACTTTTGATGCCCTGATGGAAAA	240	
Db	181	CCTAACATCACTGTTCATTTTAAAAAGTTTCCACTTGACACTTTTGATGCCCTGATGGAAAA	240	
Qy	241	CGCATATCTGGGACAGTAGAAGGGCTTCATCATATATCAATGCAACGTACAAAGAAATA	300	
Db	241	CGCATATCTGGGACAGTAGAAGGGCTTCATCATATCAATGCAACGTACAAAGAAATA	300	
Qy	301	GGGCTTCTGACCTGTGGAAGCAACAGTCAATGGGCAATTTGTATAAGACAAACTATCTCACA	360	
Db	301	GGGCTTCTGACCTGTGGAAGCAACAGTCAATGGGCAATTTGTATAAGACAAACTATCTCACA	360	
Qy	361	CATCGACAAACCAATAACAATCATAGATGTGGTTCCTGAGTCCGCTCTCATGGAAATTTGAAC	420	
Db	361	CATCGACAAACCAATAACAATCATAGATGTGGTTCCTGAGTCCGCTCTCATGGAAATTTGAAC	420	
Qy	421	TCGTGTTGGAGAAAGCTTTGTCTTAAATTTGATACAGCAAGAACTGAACTAAATGTGGGGATT	480	
Db	421	TCGTGTTGGAGAAAGCTTTGTCTTAAATTTGATACAGCAAGAACTGAACTAAATGTGGGGATT	480	

RESULT 6

RES001 6  
US-10-880-021-9  
; Sequence 9, Application US/10880021  
; Publication No. US20050043236A1  
; GENERAL INFORMATION:  
; APPLICANT: Daly, Thomas J.  
; APPLICANT: Fandl, James P.  
; APPLICANT: Papadopoulos, Nicholas J.  
; TITLE OF INVENTION: VEGF Traps and Therapeutic Uses Thereof  
; FILE REFERENCE: RGE 710D2  
; CURRENT APPLICATION NUMBER: US/10/880, 021

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; CURRENT FILING DATE: 2004-06-29
; PRIOR APPLICATION NUMBER: 10/609,775
; FILING DATE: 2003-06-30
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1377
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-880-021-9

Query Match      100.0%; Score 1377; DB 21; Length 1377;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTCAGCTACTGGGACACCGGGTCTCTGTGCGCGCTGCTCAGCTGCTCTCTC 60
Db 1 ATGTCAGCTACTGGGACACCGGGTCTCTGTGCGCGCTGCTCAGCTGCTCTCTC 60

Qy 61 ACAGATCTAGTTCGGGAGTGATACCGGTAGACCTTTCGTAGAGATGACAGTGAATC 120
Db 61 ACAGATCTAGTTCGGGAGTGATACCGGTAGACCTTTCGTAGAGATGACAGTGAATC 120

Qy 121 CCCGAAATTTATACATGACTGAAGGAGGAGCTCGTCAATTCCTGCGGGTTACGTCA 180
Db 121 CCCGAAATTTATACATGACTGAAGGAGGAGCTCGTCAATTCCTGCGGGTTACGTCA 180

Qy 181 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACATTTGATCCCTGATGGAATA 240
Db 181 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACATTTGATCCCTGATGGAATA 240

Qy 241 CGCATATCTGGGACAGTGAAGGGCTTCATCATATCAATGCAAGTCAAGAGAATA 300
Db 241 CGCATATCTGGGACAGTGAAGGGCTTCATCATATCAATGCAAGTCAAGAGAATA 300

Qy 301 GGGCTTCTGACTGTGAAGCAACAGTCAATGGGCAATTTGTATAAGACAAACTTCTACA 360
Db 301 GGGCTTCTGACTGTGAAGCAACAGTCAATGGGCAATTTGTATAAGACAAACTTCTACA 360

Qy 361 CATCGACAAACCAATACAAATCATAGATGTGTTCTGAGTCGGTCTCATGGAATTTGAATA 420
Db 361 CATCGACAAACCAATACAAATCATAGATGTGTTCTGAGTCGGTCTCATGGAATTTGAATA 420

Qy 421 TCTGTTGAGAAAAGCTTGTCTTAAATTTGTACAGCAAGAACTGAATTAATGTTGGGATT 480
Db 421 TCTGTTGAGAAAAGCTTGTCTTAAATTTGTACAGCAAGAACTGAATTAATGTTGGGATT 480

Qy 481 GACTTCAACTGGGAATACCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 540
Db 481 GACTTCAACTGGGAATACCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 540

Qy 541 CTAATAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGTAGCACCTTAATATAGATGGT 600
Db 541 CTAATAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGTAGCACCTTAATATAGATGGT 600

Qy 601 GTAACCCGGAGTGACCAAGGATTTGACACCTGTGAGCATCCAGTGGGCTGATGCCAAG 660
Db 601 GTAACCCGGAGTGACCAAGGATTTGACACCTGTGAGCATCCAGTGGGCTGATGCCAAG 660

Qy 661 AAGAACAGACATTTGTGAGGGTCCATGAAAGAGCAAAATCTACACATGCCACCGTGC 720
Db 661 AAGAACAGACATTTGTGAGGGTCCATGAAAGAGCAAAATCTACACATGCCACCGTGC 720

Qy 721 CCAGACCTGAATCTCTGGGGGACCGTCACTGTTCTCTTTCCCGCCCAAAACCCAAAGGAC 780
Db 721 CCAGACCTGAATCTCTGGGGGACCGTCACTGTTCTCTTTCCCGCCCAAAACCCAAAGGAC 780

Qy 781 ACCCTCATGATCTCCCGGACCCCTGAGTTCATGCTGCTGCTGGTGGAGTGAAGCAAG 840
Db 781 ACCCTCATGATCTCCCGGACCCCTGAGTTCATGCTGCTGCTGGTGGAGTGAAGCAAG 840

Qy 841 GACCTCGAGGTCAGTTCAACTGTTACGTGAGCGGCTGGAGGTCATTAATGCCAAGACA 900
Db 841 GACCTCGAGGTCAGTTCAACTGTTACGTGAGCGGCTGGAGGTCATTAATGCCAAGACA 900
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Db 841 GACCTCGAGGTCAGTTCAACTGTTACGTGAGCGGCTGGAGGTCATTAATGCCAAGACA 900
Qy 901 AAGCCGGGAGGAGCAGTACAACAGCAGTACCGTGTGGTACAGCTCTTACCGTCTCTG 960
Db 901 AAGCCGGGAGGAGCAGTACAACAGCAGTACCGTGTGGTACAGCTCTTACCGTCTCTG 960
Qy 961 CACGAGACTGGCTGAATGCAAGGAGTACAAGTGAAGTCTTCCAAAGAGCCCTCCCA 1020
Db 961 CACGAGACTGGCTGAATGCAAGGAGTACAAGTGAAGTCTTCCAAAGAGCCCTCCCA 1020
Qy 1021 GCCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGAACACACAGGTGTAC 1080
Db 1021 GCCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCGAGAACACACAGGTGTAC 1080
Qy 1081 ACCCTGCCCCATCCCGGATGAGTGAACAAAGAACAGGTACAGCTGCTGGTCTC 1140
Db 1081 ACCCTGCCCCATCCCGGATGAGTGAACAAAGAACAGGTACAGCTGCTGGTCTC 1140
Qy 1141 AAAGGCTTCTATCCAGGACATCGCGTGGAGTGGGAGAGCAATGGGAGCCCGGAAC 1200
Db 1141 AAAGGCTTCTATCCAGGACATCGCGTGGAGTGGGAGAGCAATGGGAGCCCGGAAC 1200
Qy 1201 AACTACAGAACCCAGCTCCCGTGGACTCCGACGGCTCTTCTTCTCTACAGCAAG 1260
Db 1201 AACTACAGAACCCAGCTCCCGTGGACTCCGACGGCTCTTCTTCTCTACAGCAAG 1260
Qy 1261 CTACCCGTGACAAAGAGCAGGTGGCAGAGGGGAACGTCTTCTCATGCTCGGTGATGAT 1320
Db 1261 CTACCCGTGACAAAGAGCAGGTGGCAGAGGGGAACGTCTTCTCATGCTCGGTGATGAT 1320
Qy 1321 GAGGCTCTGCACACCACTACAGCAGAGAGCTCTCCCTGTCTCCGGGTAAATGA 1377
Db 1321 GAGGCTCTGCACACCACTACAGCAGAGAGCTCTCCCTGTCTCCGGGTAAATGA 1377

RESULT 7
US-10-909-011-3
; Sequence 3, Application US/10909011
; Publication No. US2005012061A1
; GENERAL INFORMATION:
; APPLICANT: Jocelyn Helash
; APPLICANT: George Vancopoulos
; APPLICANT: Phyllis R. Wachsbarger
; APPLICANT: Adam P. Dicker
; APPLICANT: Randy Burd
; TITLE OF INVENTION: Use of a VEGF Antagonist in Combination with Radiation Therapy
; FILE REFERENCE: REG 716A
; CURRENT APPLICATION NUMBER: US/10/909,011
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/492,864
; PRIOR FILING DATE: 2003-08-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1377
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-909-011-3

Query Match      100.0%; Score 1377; DB 21; Length 1377;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTCAGCTACTGGGACACCGGGTCTCTGTGCGCGCTGCTCAGCTGCTCTCTC 60
Db 1 ATGTCAGCTACTGGGACACCGGGTCTCTGTGCGCGCTGCTCAGCTGCTCTCTC 60

Qy 61 ACAGATCTAGTTCGGGAGTGATACCGGTAGACCTTTCGTAGAGATGACAGTGAATC 120
Db 61 ACAGATCTAGTTCGGGAGTGATACCGGTAGACCTTTCGTAGAGATGACAGTGAATC 120

Qy 121 CCCGAAATTTATACATGACTGAAGGAGGAGCTCGTCAATTCCTGCGGGTTACGTCA 180
Db 121 CCCGAAATTTATACATGACTGAAGGAGGAGCTCGTCAATTCCTGCGGGTTACGTCA 180

Qy 181 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACATTTGATCCCTGATGGAATA 240
Db 181 CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACATTTGATCCCTGATGGAATA 240

Qy 241 CGCATATCTGGGACAGTGAAGGGCTTCATCATATCAATGCAAGTCAAGAGAATA 300
Db 241 CGCATATCTGGGACAGTGAAGGGCTTCATCATATCAATGCAAGTCAAGAGAATA 300

Qy 301 GGGCTTCTGACTGTGAAGCAACAGTCAATGGGCAATTTGTATAAGACAAACTTCTACA 360
Db 301 GGGCTTCTGACTGTGAAGCAACAGTCAATGGGCAATTTGTATAAGACAAACTTCTACA 360

Qy 361 CATCGACAAACCAATACAAATCATAGATGTGTTCTGAGTCGGTCTCATGGAATTTGAATA 420
Db 361 CATCGACAAACCAATACAAATCATAGATGTGTTCTGAGTCGGTCTCATGGAATTTGAATA 420

Qy 421 TCTGTTGAGAAAAGCTTGTCTTAAATTTGTACAGCAAGAACTGAATTAATGTTGGGATT 480
Db 421 TCTGTTGAGAAAAGCTTGTCTTAAATTTGTACAGCAAGAACTGAATTAATGTTGGGATT 480

Qy 481 GACTTCAACTGGGAATACCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 540
Db 481 GACTTCAACTGGGAATACCTTCTTCGAAGCATCAGCATAAGAAACTTGTAAACCGAGAC 540

Qy 541 CTAATAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGTAGCACCTTAATATAGATGGT 600
Db 541 CTAATAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGTAGCACCTTAATATAGATGGT 600

Qy 601 GTAACCCGGAGTGACCAAGGATTTGACACCTGTGAGCATCCAGTGGGCTGATGCCAAG 660
Db 601 GTAACCCGGAGTGACCAAGGATTTGACACCTGTGAGCATCCAGTGGGCTGATGCCAAG 660

Qy 661 AAGAACAGACATTTGTGAGGGTCCATGAAAGAGCAAAATCTACACATGCCACCGTGC 720
Db 661 AAGAACAGACATTTGTGAGGGTCCATGAAAGAGCAAAATCTACACATGCCACCGTGC 720

Qy 721 CCAGACCTGAATCTCTGGGGGACCGTCACTGTTCTCTTTCCCGCCCAAAACCCAAAGGAC 780
Db 721 CCAGACCTGAATCTCTGGGGGACCGTCACTGTTCTCTTTCCCGCCCAAAACCCAAAGGAC 780

Qy 781 ACCCTCATGATCTCCCGGACCCCTGAGTTCATGCTGCTGCTGGTGGAGTGAAGCAAG 840
Db 781 ACCCTCATGATCTCCCGGACCCCTGAGTTCATGCTGCTGCTGGTGGAGTGAAGCAAG 840

Qy 841 GACCTCGAGGTCAGTTCAACTGTTACGTGAGCGGCTGGAGGTCATTAATGCCAAGACA 900
Db 841 GACCTCGAGGTCAGTTCAACTGTTACGTGAGCGGCTGGAGGTCATTAATGCCAAGACA 900
```

Db 121 CCCGAAATTATACATGACTGAAGAGGAGGAGCTCGTCATTCCCTCGCGGGTTACGTCA 180  
Qy 181 CTTAATCATCTGTTACTTTAAAAAGTTTCCACTTTCACACTTTGATCCCTGATGAAAA 240  
Db 181 CTTAATCATCTGTTACTTTAAAAAGTTTCCACTTTCACACTTTGATCCCTGATGAAAA 240  
Qy 241 CGCATATCTGGGACAGTAGAAGGGCTTCATCATATCAAAATGCAAAAGAAATA 300  
Db 241 CGCATATCTGGGACAGTAGAAGGGCTTCATCATATCAAAATGCAAAAGAAATA 300  
Qy 301 GGGCTTCGACCTGTGAAGCACAGTCAATGGCATTGTTATAGACAAACTATCTCACA 360  
Db 301 GGGCTTCGACCTGTGAAGCACAGTCAATGGCATTGTTATAGACAAACTATCTCACA 360  
Qy 361 CATCGACAAACCAATACATATAGATGTGTTCTGAGTCCGTCTCATCGAAATGAACTA 420  
Db 361 CATCGACAAACCAATACATATAGATGTGTTCTGAGTCCGTCTCATCGAAATGAACTA 420  
Qy 421 TCTGTTGAGAAAAAGCTTGTCTTAAATTTGTACAGCAAGACTGAACTAAATGTGGGATT 480  
Db 421 TCTGTTGAGAAAAAGCTTGTCTTAAATTTGTACAGCAAGACTGAACTAAATGTGGGATT 480  
Qy 481 GACTTCACTGGGATACCTCTTCGAGCATCAGCATAGCAAGAACTTGTAAACCGAGAC 540  
Db 481 GACTTCACTGGGATACCTCTTCGAGCATCAGCATAGCAAGAACTTGTAAACCGAGAC 540  
Qy 541 CTAACAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGGACACCTTAACATATAGATGGT 600  
Db 541 CTAACAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGGACACCTTAACATATAGATGGT 600  
Qy 601 GTAAACCCGAGTGACCAAGGATTTGACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660  
Db 601 GTAAACCCGAGTGACCAAGGATTTGACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660  
Qy 661 AAGAACAGCATTGTCAGGGTCCATGAAGAGCAAAACTCACAATGCCACCGTGC 720  
Db 661 AAGAACAGCATTGTCAGGGTCCATGAAGAGCAAAACTCACAATGCCACCGTGC 720  
Qy 721 CCAGCAGCTGAATCTCGGGGGACCGTCAGTCTTCCTTCCTCCCAACCAAGGAC 780  
Db 721 CCAGCAGCTGAATCTCGGGGGACCGTCAGTCTTCCTTCCTCCCAACCAAGGAC 780  
Qy 781 ACCCTCATGATCTCCCGGACCCCTGAGGTCAATGCGTGGTGGAGCGTGAGCCACGAA 840  
Db 781 ACCCTCATGATCTCCCGGACCCCTGAGGTCAATGCGTGGTGGAGCGTGAGCCACGAA 840  
Qy 841 GACCTGAGGTCAAGTTCACTGTAAGTCAATGCGTGGTGGAGCGTGAGTGCATATGCCAAGACA 900  
Db 841 GACCTGAGGTCAAGTTCACTGTAAGTCAATGCGTGGTGGAGCGTGAGTGCATATGCCAAGACA 900  
Qy 901 AAGCCGGGAGGAGCAGTACAAAGCAGCAGTACCGTGTGGTTCAGCTCCTCACCGTCTGT 960  
Db 901 AAGCCGGGAGGAGCAGTACAAAGCAGCAGTACCGTGTGGTTCAGCTCCTCACCGTCTGT 960  
Qy 961 CACCAAGGATCGGCTGAATGGCAAGAGTCAAGTGCAGAGTCTCCAAAGAGCCCTCCCA 1020  
Db 961 CACCAAGGATCGGCTGAATGGCAAGAGTCAAGTGCAGAGTCTCCAAAGAGCCCTCCCA 1020  
Qy 1021 GCGCCCATCGAGAAAAACATCTCCAAAGCCAAAGGCGAGCCCGAGAACCAACAGGTGTAC 1080  
Db 1021 GCGCCCATCGAGAAAAACATCTCCAAAGCCAAAGGCGAGCCCGAGAACCAACAGGTGTAC 1080  
Qy 1081 ACCCTGCCCCCATCCCGGGATGAGTGAACAGCAAGCAAGTTCAGCTGACCTGCTCGTCT 1140  
Db 1081 ACCCTGCCCCCATCCCGGGATGAGTGAACAGCAAGCAAGTTCAGCTGACCTGCTCGTCT 1140  
Qy 1141 AAAGGCTTCTATCCAGGACATCGCCGTGGAGTGGAGAGCAATGGGCGAGCCCGAGAAC 1200  
Db 1141 AAAGGCTTCTATCCAGGACATCGCCGTGGAGTGGAGAGCAATGGGCGAGCCCGAGAAC 1200  
Qy 1201 AACTAAGACCAAGCTCCCGTGTGAGTCCGAGCGGCTCTTCTTCTCTTACAGCAAG 1260  
Db 1201 AACTAAGACCAAGCTCCCGTGTGAGTCCGAGCGGCTCTTCTTCTCTTACAGCAAG 1260

RESULT 8

US-10-988-243-15  
; Sequence 15, Application US/10988243  
; Publication No. US20050175610A1  
; GENERAL INFORMATION:  
; APPLICANT: Wiegand, Stanley  
; APPLICANT: Papadopoulos, Nicholas J.  
; APPLICANT: Yancopoulos, George  
; TITLE OF INVENTION: Modified Chimeric Polypeptides with Improved Pharmacokinetic Properties  
; TITLE OF INVENTION: and Methods of Making and Using Thereof  
; FILE REFERENCE: REG 710F  
; CURRENT APPLICATION NUMBER: US/10/988,243  
; CURRENT FILING DATE: 2004-11-12  
; PRIOR APPLICATION NUMBER: 10/009,852  
; PRIOR FILING DATE: 2001-12-06  
; PRIOR APPLICATION NUMBER: PCT/US00/14142  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/138,133  
; PRIOR FILING DATE: 1999-06-08  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15  
; LENGTH: 1377  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-988-243-15

Query Match 100.0%; Score 1377; DB 22; Length 1377;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTCAGCTACTCGGACACCGGGTCTCTGCTGCGCGTGTCTCAGCTGTCTGCTTCTC 60  
Db 1 ATGTCAGCTACTCGGACACCGGGTCTCTGCTGCGCGTGTCTCAGCTGTCTGCTTCTC 60  
Qy 61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAATC 120  
Db 61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAATC 120  
Qy 121 CCCGAAATTATACATGACTGAAGAGGAGGAGCTCGTCATTCCCTGCGGGTTACGTCA 180  
Db 121 CCCGAAATTATACATGACTGAAGAGGAGGAGCTCGTCATTCCCTGCGGGTTACGTCA 180  
Qy 181 CCTAATCATCTGTTACTTTTAAAAAGTTTCCACTTTCACACTTTGATCCCTGATGAAAA 240  
Db 181 CCTAATCATCTGTTACTTTTAAAAAGTTTCCACTTTCACACTTTGATCCCTGATGAAAA 240  
Qy 241 CGCATATCTGGGACAGTAGAAGGGCTTCATCATATCAAAATGCAAAAGAAATA 300  
Db 241 CGCATATCTGGGACAGTAGAAGGGCTTCATCATATCAAAATGCAAAAGAAATA 300  
Qy 301 GGGCTTCGACCTGTGAAGCAACAGTCAATGGGCAATTTGTATAGACAAACTATCTCACA 360  
Db 301 GGGCTTCGACCTGTGAAGCAACAGTCAATGGGCAATTTGTATAGACAAACTATCTCACA 360  
Qy 361 CATCGACAAACCAATACATATAGATGTGTTCTGAGTCCGTCTCATGGAAATGAACTA 420  
Db 361 CATCGACAAACCAATACATATAGATGTGTTCTGAGTCCGTCTCATGGAAATGAACTA 420  
Qy 421 TCTGTTGAGAAAAAGCTTGTCTTAAATTTGTACAGCAAGAACTGAACTAAATGTGGGATT 480  
Db 421 TCTGTTGAGAAAAAGCTTGTCTTAAATTTGTACAGCAAGAACTGAACTAAATGTGGGATT 480







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Qy 841 GACCTGAGGTCAAGTTCAACTGGTACGTGGACCGCGTGGAGGTGCATAATGCCAAGACA 900
Db 841 GACCTGAGGTCAAGTTCAACTGGTACGTGGACCGCGTGGAGGTGCATAATGCCAAGACA 900
Qy 901 AAGCGCGGGAGGAGCAGTACAACAGCAGCTACCGTGTGGTTCAGGCTCCTCACGTCCTG 960
Db 901 AAGCGCGGGAGGAGCAGTACAACAGCAGCTACCGTGTGGTTCAGGCTCCTCACGTCCTG 960
Qy 961 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAGAGTCTCCAAACAAAGCCCTCCCA 1020
Db 961 CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAGAGTCTCCAAACAAAGCCCTCCCA 1020
Qy 1021 GCGCCCATCGAGAAAAACCATCTCCAAAGCCAAAGCGGAGCCCGGAGAACACACAGGTGTAC 1080
Db 1021 GCGCCCATCGAGAAAAACCATCTCCAAAGCCAAAGCGGAGCCCGGAGAACACACAGGTGTAC 1080
Qy 1081 ACCCTGCCCCCATCCCGGATGAGTGCACCAAGAACAGGTGACGCTGACCTGCTGGTC 1140
Db 1081 ACCCTGCCCCCATCCCGGATGAGTGCACCAAGAACAGGTGACGCTGACCTGCTGGTC 1140
Qy 1141 AAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGACGCCGAGAAC 1200
Db 1141 AAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGACGCCGAGAAC 1200
Qy 1201 AACTACAAGACCAACGCTCCGCTGCTGAGTCCGACCGGCTCTCTCTCTACAGCAAG 1260
Db 1201 AACTACAAGACCAACGCTCCGCTGCTGAGTCCGACCGGCTCTCTCTCTACAGCAAG 1260
Qy 1261 CTACCGTGGACAAGAGCAGTGGCAGCAGGGGAAAGTCTTCTCATGCTCCGTCATGCAT 1320
Db 1261 CTACCGTGGACAAGAGCAGTGGCAGCAGGGGAAAGTCTTCTCATGCTCCGTCATGCAT 1320
Qy 1321 GAGGCTCTGCACAAACCACTACACGACAGAGCCTCTCCCTGCTCCCGGTAAATGA 1377
Db 1321 GAGGCTCTGCACAAACCACTACACGACAGAGCCTCTCCCTGCTCCCGGTAAATGA 1377
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## RESULT 10

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US-11-016-097-15
; Sequence 15, Application US/11016097
; Publication No. US20050163798A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Papadopoulos et al.
; TITLE OF INVENTION: MODIFIED CHIMERIC POLYPEPTIDES WITH IMPROVED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING THEREOF
; FILE REFERENCE: REG 710-A-US
; CURRENT APPLICATION NUMBER: US/11/016.097
; CURRENT FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: US/10/009,852
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/14142
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/139,133
; PRIOR FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 1377
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1374)
US-11-016-097-15
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Query Match 100.0%; Score 1377; DB 24; Length 1377;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCTCAGCTACTGGGACACCGGGGTCCTGTCGCGCTGCTCAGCTGCTGCTCTC 60
|
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Db 1 ATGCTCAGCTACTGGGACACCGGGGTCCTGTCGCGCTGCTCAGCTGCTGCTCTC 60
Qy 61 ACAGATCTAGTTCGCGAAGTGATACCGGTAGACCTTTTCGTAGAGATGTACAGTGAATC 120
|
Db 61 ACAGATCTAGTTCGCGAAGTGATACCGGTAGACCTTTTCGTAGAGATGTACAGTGAATC 120
|
Qy 121 CCGGAAATTTACACATGACTGAAGAGGAGGAGCTCGTCAATTCCTGCGGGTTACGTCA 180
|
Db 121 CCGGAAATTTACACATGACTGAAGAGGAGGAGCTCGTCAATTCCTGCGGGTTACGTCA 180
|
Qy 181 CCTAACATCACTGTTACTTTAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAATA 240
|
Db 181 CCTAACATCACTGTTACTTTAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAATA 240
|
Qy 241 CGCATATCTGGGACAGTAGAAAGGGCTTCATCATATCAAAATGCAACGTACAAGAAATA 300
|
Db 241 CGCATATCTGGGACAGTAGAAAGGGCTTCATCATATCAAAATGCAACGTACAAGAAATA 300
|
Qy 301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360
|
Db 301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360
|
Qy 361 CATCGACAAACCAATACAATCATAGATGTGGTCTGAGTCCGTCTCATGGAATTTGAAC 420
|
Db 361 CATCGACAAACCAATACAATCATAGATGTGGTCTGAGTCCGTCTCATGGAATTTGAAC 420
|
Qy 421 TCTGTTGGAGAAAAGCTTGTCTTAAATTTGTACACAAAGAACTGAACCTAAATGTGGGAT 480
|
Db 421 TCTGTTGGAGAAAAGCTTGTCTTAAATTTGTACACAAAGAACTGAACCTAAATGTGGGAT 480
|
Qy 481 GACTTCAACTGGGAATACCTCTTTCGAAGCATCAGCATTAAGAAACTTTGTAACCGAGAC 540
|
Db 481 GACTTCAACTGGGAATACCTCTTTCGAAGCATCAGCATTAAGAAACTTTGTAACCGAGAC 540
|
Qy 541 CTAAAAACCCAGCTCTGGGAGTGAAGAAATTTTGGAGCACCTTAATCTATAGATGGT 600
|
Db 541 CTAAAAACCCAGCTCTGGGAGTGAAGAAATTTTGGAGCACCTTAATCTATAGATGGT 600
|
Qy 601 GTAAACCGGAGTGACCAAGGATTTGTACACCTGTGCAGCATCCAGTGGCTGATGACCAAG 660
|
Db 601 GTAAACCGGAGTGACCAAGGATTTGTACACCTGTGCAGCATCCAGTGGCTGATGACCAAG 660
|
Qy 661 AAGAACACGACATTTGTTCAGGCTCCATGAAAGAGCAAAACTCACATGCCACCGTGC 720
|
Db 661 AAGAACACGACATTTGTTCAGGCTCCATGAAAGAGCAAAACTCACATGCCACCGTGC 720
|
Qy 721 CCAGCACCTGAACTCTCTGGGGGACCGTCACTCTTCTTCCCCCAAAACCCCAAGGAC 780
|
Db 721 CCAGCACCTGAACTCTCTGGGGGACCGTCACTCTTCTTCCCCCAAAACCCCAAGGAC 780
|
Qy 781 ACCCTCATGATCTCCCGGACCCCTGAGGTCAATGCGTGGTGGGAGCGTGAGCCACGAA 840
|
Db 781 ACCCTCATGATCTCCCGGACCCCTGAGGTCAATGCGTGGTGGGAGCGTGAGCCACGAA 840
|
Qy 841 GACCTGAGGTCAAGTTCAACTGCTGAGCGGCTGAGGAGTGCATTAATGCCAAGACA 900
|
Db 841 GACCTGAGGTCAAGTTCAACTGCTGAGCGGCTGAGGAGTGCATTAATGCCAAGACA 900
|
Qy 901 AAGCGCGGGAGGAGCAGTACAACAGCAGCTACCGTGTGGTTCAGGCTCCTCACGTCCTG 960
|
Db 901 AAGCGCGGGAGGAGCAGTACAACAGCAGCTACCGTGTGGTTCAGGCTCCTCACGTCCTG 960
|
Qy 961 CACGAGGACTGGCTGAATGCAAGGAGTACAAGTGCAGAGGTCTCCAAACAAAGCCCTCCCA 1020
|
Db 961 CACGAGGACTGGCTGAATGCAAGGAGTACAAGTGCAGAGGTCTCCAAACAAAGCCCTCCCA 1020
|
Qy 1021 GCGCCCATCGAGAAAAACCATCTCCAAAGCCAAAGCGGAGCCCGGAGAACACACAGGTGTAC 1080
|
Db 1021 GCGCCCATCGAGAAAAACCATCTCCAAAGCCAAAGCGGAGCCCGGAGAACACACAGGTGTAC 1080
|
Qy 1081 ACCCTGCCCCCATCCCGGATGAGTGCACCAAGAACAGGTGACGCTGACCTGCTGGTC 1140
|
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|
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D	b	840	CCCAAGGACACCCTTCATGATCTCCCGACCCCTGAGGTCACTGCGTGGTGAGCATGTG	899
O	y	832	AGGCACAAGAACCCTTGAGGTCAAGTTCAA	891
D	b	900	AGCACGAAGCCTTGAGGTCAAGTTCAA	959
O	y	892	GCCAAGACAAGCCGCGGAGGAGCAGTACA	951
D	b	960	GCCAAGACAAGCCGCGGAGGAGCAGTACA	1019
O	y	952	ACCGTCTGACACAGGACTCGCTGAATG	1011
D	b	1020	ACCGTCTGACACAGGACTCGCTGAATG	1079
O	y	1012	GCCCTCCAGCCCCCATCGAAGAAACCAT	1071
D	b	1080	GCCCTCCAGCCCCCATCGAAGAAACCAT	1139
O	y	1072	CAGGTGTACACCTGCCCCCATTCCCGGAT	1131
D	b	1140	CAGGTGTACACCTGCCCCCATTCCCGGAT	1199
O	y	1132	TGCGTGTCAAAGGCTTCTATCCAGCGCAT	1191
D	b	1200	TGCGTGTCAAAGGCTTCTATCCAGCGCAT	1259
O	y	1192	CCGAGAGAACACTACAAAGACACCGCT	1251
D	b	1260	CCGAGAGAACACTACAAAGACACCGCT	1319
O	y	1252	TACAGCAAGCTCACCGTGGACAAGAGCA	1311
D	b	1320	TATAGCAAGCTCACCGTGGACAAGAGCA	1379
O	y	1312	GTGATGATGAGGCTGTGCAACAACCACTA	1371
D	b	1380	GTGATGATGAGGCTGTGCAACAACCACTA	1439
O	y	1372	AAATGA 1377	
D	b	1440	AAATGA 1445	
 RESULT 13 US-10-609-775-7 ; Sequence 7, Application US/10609775 ; Publication No. US20040014667A1 ; GENERAL INFORMATION: ; APPLICANT: Thomas J. Daly ; APPLICANT: Nicholas J. Papadopoulos ; TITLE OF INVENTION: VEGF TRAPS AND THERAPEUTIC USES THEREOF ; FILE OF INVENTION: REG 710D ; CURRENT FILING DATE: 2003-06-30 ; PRIOR APPLICATION NUMBER: US/10/609,775 ; PRIOR FILING DATE: 2003-06-30 ; PRIOR APPLICATION NUMBER: 10/009,852 ; PRIOR FILING DATE: 2001-12-06 ; PRIOR APPLICATION NUMBER: PCT/US00/14142 ; PRIOR FILING DATE: 2000-05-23 ; PRIOR APPLICATION NUMBER: 60/138,133 ; PRIOR FILING DATE: 1999-06-08 ; NUMBER OF SEQ ID NOS: 25 ; SOFTWARE: FastSeq for Windows Version 4.0 ; SEQ ID NO 7 ; LENGTH: 1453 ; TYPE: DNA ; ORGANISM: homo sapiens US-10-609-775-7				
 Query Match      96.5%; Score 1328.4; DB 17; Length 1453; Best Local Similarity 98.6%; Pred. No. 0; Matches 1367; Conservative 0; Mismatches 1; Indels 18; Gaps 2;				

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QY 1 ATGTCAGCTACTGGGACACCGGGTCTCTGTGTGCGCGTGTCTAGCTGTCTGCTTCTC 60
Db 69 ATGTCAGCTACTGGGACACCGGGTCTCTGTGTGCGCGTGTCTAGCTGTCTGCTTCTC 128
QY 61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTTCGTAGAGATGTACAGTGAATC 120
Db 129 ACAGGATCTAGTTCCGGA-----GGTAGACCTTTTCGTAGAGATGTACAGTGAATC 179
QY 121 CCCGAAATTATACATGACTGAGGAAGGAGCTCGTCAATCCCTGCCGGGTTACGTCA 180
Db 180 CCCGAAATTATACATGACTGAGGAAGGAGCTCGTCAATCCCTGCCGGGTTACGTCA 239
QY 181 CTTAACTACTGTTACTTTAAAGGTTTCCACTTGACACTTTTGATCCCTGTATGGAATA 240
Db 240 CTTAACTACTGTTACTTTAAAGGTTTCCACTTGACACTTTTGATCCCTGTATGGAATA 299
QY 241 CGCATAATCTGGGACAGTAGAAGGGCTTCATCATATCAATCAATGCAACGTACAAGAAATA 300
Db 300 CGCATAATCTGGGACAGTAGAAGGGCTTCATCATATCAATGCAACGTACAAGAAATA 359
QY 301 GGGCTTCTGACCTGTGGAAGCAACAGTCAATGGGCAATTTGTAAAGACAAACTATCTCACA 360
Db 360 GGGCTTCTGACCTGTGGAAGCAACAGTCAATGGGCAATTTGTAAAGACAAACTATCTCACA 419
QY 361 CATCGACAAACCAATACATATAGATGTGGTCTGAGTCCGCTCATGGAATGAACTA 420
Db 420 CATCGACAAACCAATACATATAGATGTGGTCTGAGTCCGCTCATGGAATGAACTA 479
QY 421 TCTGTTGGAGAAAGCTTGTCTTAAATTTGACAGCAAGAACTGAACTAAATGTGGGATT 480
Db 480 TCTGTTGGAGAAAGCTTGTCTTAAATTTGACAGCAAGAACTGAACTAAATGTGGGATT 539
QY 481 GACTTCAACTGGGAATACCTCTTTCGAAGCATCAGCATAGAAGAACTTTGAAACCCGAGAC 540
Db 540 GACTTCAACTGGGAATACCTCTTTCGAAGCATCAGCATAGAAGAACTTTGAAACCCGAGAC 599
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Db 600 CTAAGAACCCAGCTCTGGAGTGAGATGAAGAAATTTTGTAGACACCTTAACTATAGATGGT 659
QY 601 GTAAACCCGAGTACCAAGGATTTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660
Db 660 GTAAACCCGAGTACCAAGGATTTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 719
QY 661 AAGAACAGCATTGTTCAGGGTCCATGAAAG-----GACAAACTCACAATGC 711
Db 720 AAGAACAGCATTGTTCAGGGTCCATGAAAGGGCCCGGCGACAAACTCACAATGC 779
QY 712 CCACCGTCCCGAGCACCTGAACTCTCTGGGGGACCGTCACTTCTCTTCCCGCCCAAAA 771
Db 780 CCACCGTCCCGAGCACCTGAACTCTCTGGGGGACCGTCACTTCTCTTCCCGCCCAAAA 839
QY 772 CCAAGGACACCTCATGATCTCCCGACCCCTCAGGTTCACATCGGTGGTGGTGGAGCTG 831
Db 840 CCAAGGACACCTCATGATCTCCCGACCCCTCAGGTTCACATCGGTGGTGGTGGAGCTG 899
QY 832 AGCCACGAAGACCTTGAGGTCAAGTTCAACTGGTACGTGGACCGCGTGGAGGTGCATAAT 891
Db 900 AGCCACGAAGACCTTGAGGTCAAGTTCAACTGGTACGTGGACCGCGTGGAGGTGCATAAT 959
QY 892 GCCAAGACAAAGCCCGGAGGAGCAGTACAACAGCAGTACCGTGTGGTCAAGCTCTC 951
Db 960 GCCAAGACAAAGCCCGGAGGAGCAGTACAACAGCAGTACCGTGTGGTCAAGCTCTC 1019
QY 952 ACCGTCTGCACAGGACTGCTCAATGGCAAGAGTACAAGTGCRAAGGTCTCCACAAA 1011
Db 1020 ACCGTCTGCACAGGACTGCTCAATGGCAAGAGTACAAGTGCRAAGGTCTCCACAAA 1079
QY 1012 GCCCTCCAGCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGCGACGCCCGAGAACCA 1071
Db 1080 GCCCTCCAGCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGCGACGCCCGAGAACCA 1139
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Db 1140 CAGGTGTACACCTTGCCTCCCATCCCGGATAGCTGACCAAGAACAGGTCAGCCTGACC 1199
QY 1132 TGCTCTGGTCAAAAGGCTTCTATCCAGCGACATCGCGTGGAGTGGGAGAGCAATGGGAG 1191
Db 1200 TGCTCTGGTCAAAAGGCTTCTATCCAGCGACATCGCGTGGAGTGGGAGAGCAATGGGAG 1259
QY 1192 CCGAGAACAACTACAAGACCAAGCTCCCGTCTCGACTCGGACCGGCTCTCTCATGCTCC 1251
Db 1260 CCGAGAACAACTACAAGACCAAGCTCCCGTCTCGACTCGGACCGGCTCTCTCATGCTCC 1319
QY 1252 TACAGCAAGCTCACCGTGGACAGAGAGTGGCAGACAGGGGAACTCTCTCATGCTCC 1311
Db 1320 TATAGCAAGCTCACCGTGGACAGAGAGTGGCAGACAGGGGAACTCTCTCATGCTCC 1379
QY 1312 GTGATCATGAGGGCTCTGCACCAACCTACACGAGAAAGGCTCTCCCTGTCTCCGGGT 1371
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QY 1372 AAATGA 1377
Db 1440 AAATGA 1445

RESULT 14
US-10-880-021-7
; Sequence 7, Application US/10880021
; Publication No. US20050043236A1
; GENERAL INFORMATION:
; APPLICANT: Daly, Thomas J.
; APPLICANT: Fandl, James P.
; APPLICANT: Papadopoulos, Nicholas J.
; TITLE OF INVENTION: VEGF Traps and Therapeutic Uses Thereof
; FILE REFERENCE: RGE 710D2
; CURRENT APPLICATION NUMBER: US/10/880, 021
; CURRENT FILING DATE: 2004-06-29
; PRIOR APPLICATION NUMBER: 10/609, 775
; PRIOR FILING DATE: 2003-06-30
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1453
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-880-021-7

Query Match 96.5%; Score 1328.4; DB 21; Length 1453;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 1367; Conservative 0; Mismatches 1; Indels 18; Gaps 2;

QY 1 ATGTCAGCTACTGGGACACCGGGTCTCTGTGTGCGCGTGTCTAGCTGTCTGCTTCTC 60
Db 69 ATGTCAGCTACTGGGACACCGGGTCTCTGTGTGCGCGTGTCTAGCTGTCTGCTTCTC 128
QY 61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTTCGTAGAGATGTACAGTGAATC 120
Db 129 ACAGGATCTAGTTCCGGA-----GGTAGACCTTTTCGTAGAGATGTACAGTGAATC 179
QY 121 CCCGAAATTATACATGACTGAGGAAGGAGCTCGTCAATCCCTGCCGGGTTACGTCA 180
Db 180 CCCGAAATTATACATGACTGAGGAAGGAGCTCGTCAATCCCTGCCGGGTTACGTCA 239
QY 181 CTTAACTACTGTTACTTTAAAGGTTTCCACTTTGACACTTTTGATCCCTGTATGGAATA 240
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QY 241 CGCATAATCTGGGACAGTAGAAGGGCTTCATCATATCAATGCAACGTACAAGAAATA 300
Db 300 CGCATAATCTGGGACAGTAGAAGGGCTTCATCATATCAATGCAACGTACAAGAAATA 359
QY 301 GGGCTTCTGACCTGTGGAAGCAACAGTCAATGGGCAATTTGTAAAGACAAACTATCTCACA 360
Db 360 GGGCTTCTGACCTGTGGAAGCAACAGTCAATGGGCAATTTGTAAAGACAAACTATCTCACA 419
QY 361 CATCGACAAACCAATACATATAGATGTGGTCTGAGTCCGCTCATGGAATGAACTA 420
Db 420 CATCGACAAACCAATACATATAGATGTGGTCTGAGTCCGCTCATGGAATGAACTA 479
QY 421 TCTGTTGGAGAAAGCTTGTCTTAAATTTGACAGCAAGAACTGAACTAAATGTGGGATT 480
Db 480 TCTGTTGGAGAAAGCTTGTCTTAAATTTGACAGCAAGAACTGAACTAAATGTGGGATT 539
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Db 600 CTAAGAACCCAGCTCTGGAGTGAGATGAAGAAATTTTGTAGACACCTTAACTATAGATGGT 659
QY 601 GTAAACCCGAGTACCAAGGATTTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660
Db 660 GTAAACCCGAGTACCAAGGATTTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 719
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QY 712 CCACCGTCCCGAGCACCTGAACTCTCTGGGGGACCGTCACTTCTCTTCCCGCCCAAAA 771
Db 780 CCACCGTCCCGAGCACCTGAACTCTCTGGGGGACCGTCACTTCTCTTCCCGCCCAAAA 839
QY 772 CCAAGGACACCTCATGATCTCCCGACCCCTCAGGTTCACATCGGTGGTGGTGGAGCTG 831
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QY 832 AGCCACGAAGACCTTGAGGTCAAGTTCAACTGGTACGTGGACCGCGTGGAGGTGCATAAT 891
Db 900 AGCCACGAAGACCTTGAGGTCAAGTTCAACTGGTACGTGGACCGCGTGGAGGTGCATAAT 959
QY 892 GCCAAGACAAAGCCCGGAGGAGCAGTACAACAGCAGTACCGTGTGGTCAAGCTCTC 951
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QY 952 ACCGTCTGCACAGGACTGCTCAATGGCAAGAGTACAAGTGCRAAGGTCTCCACAAA 1011
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QY 1012 GCCCTCCAGCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGCGACGCCCGAGAACCA 1071
Db 1080 GCCCTCCAGCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGCGACGCCCGAGAACCA 1139
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Db 600 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGTAGCACCTTAACTATAGATGGT 659
Qy 601 GTAAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660
Db 660 GTAAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 719
Qy 661 AAGAACAGCATTGTTCAGGGTCCATGAAAG-----GACAAACTCACACATGC 711
Db 720 AAGAACAGCATTGTTCAGGGTCCATGAAAGGGCCCCGGCGACAAACTCACACATGC 779
Qy 712 CCACCGTGCCAGCACCTGAACTCCTGGGGGACCGTCAGTCTTCTTCCGCCCAAAA 771
Db 780 CCACCGTGCCAGCACCTGAACTCCTGGGGGACCGTCAGTCTTCTTCCGCCCAAAA 839
Qy 772 CCCAAGGACACCTTCATGATCTCCCGGACCCCTGAGGTCAATCGTGGTGGGACGTG 831
Db 840 CCCAAGGACACCTTCATGATCTCCCGGACCCCTGAGGTCAATCGTGGTGGGACGTG 899
Qy 832 AGCCACGAAGACCTGTGAGTCAAGTTCAATCTGAGTGGAGCGGCTGGAGGTGCATAAT 891
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Qy 952 ACCGTCTCGACCAAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAGAGTCTCCAAACA 1011
Db 1020 ACCGTCTCGACCAAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAGAGTCTCCAAACA 1079
Qy 1012 GCCCTCCAGCCCCCATCGAGAAACCATCTCCAAAGCAGGAGGAGCCCGGAGAACCA 1071
Db 1080 GCCCTCCAGCCCCCATCGAGAAACCATCTCCAAAGCAGGAGGAGCCCGGAGAACCA 1139
Qy 1072 CAGGTGTACACCTTGCCTCCGATGAGCTGACCAAGAACAGGTCAGGCTGACCC 1131
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Db 1260 CCGAGAGAACCACTACAGACCAACGCTTCCGTCGTGAGCTCCGAGCGCTCTTCTCCTC 1319
Qy 1252 TACAGCAAGCTCACCGTGGGACAGAGAGTGGGAGGAGGAGGAGGCTTCTCATGCTCC 1311
Db 1320 TATAGCAAGCTCACCGTGGGACAGAGAGTGGGAGGAGGAGGAGGCTTCTCATGCTCC 1379
Qy 1312 GTGATGATGAGGCTCTGCACCAACCACTACACGAGAGAGGCTTCTCCCTGTCTCCGGGT 1371
Db 1380 GTGATGATGAGGCTCTGCACCAACCACTACACGAGAGAGGCTTCTCCCTGTCTCCGGGT 1439
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Db 1440 AATGA 1445
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## RESULT 15

US-10-909-011-1

; Sequence 1, Application US/10909011

; Publication No. US20050112061A1

; GENERAL INFORMATION:

; APPLICANT: Jocelyn Holash

; APPLICANT: George Vancopoulos

; APPLICANT: Phyllis R. Wachseberger

; APPLICANT: Adam P. Dicker

; APPLICANT: Randy Burd

; TITLE OF INVENTION: Use of a VEGF Antagonist in Combination with Radiation Therapy

; FILE REFERENCE: REG 716A

; CURRENT APPLICATION NUMBER: US/10/909,011

; CURRENT FILING DATE: 2004-07-30

; PRIOR APPLICATION NUMBER: 60/492,864

; PRIOR FILING DATE: 2003-08-06

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: Fast-Seq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 1453

; TYPE: DNA

; ORGANISM: homo sapiens

; US-10-909-011-1

Query Match 96.5%; Score 1328.4; DB 21; Length 1453;

Best Local Similarity 98.6%; Pred. No. 0;

Matches 1367; Conservative 0; Mismatches 1; Indels 18; Gaps 2;

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Qy 1 ATGGTCAAGTCTAGTGGGACACCGGGGTCCTGCTGTGCGCGTGTCTCAGCTGTCTCTTC 60
Db 69 ATGGTCAAGTCTAGTGGGACACCGGGGTCCTGCTGTGCGCGTGTCTCAGCTGTCTCTTC 128
Qy 61 ACAGGATCTAGTTCGCGAAGTGATACCGGTAGACCTTTCTGTAGAGATGTACAGTGAATC 120
Db 129 ACAGGATCTAGTTCGCGA-----GGTAGACCTTTCTGTAGAGATGTACAGTGAATC 179
Qy 121 CCCGAAATTTATACATGACTGAAAGGAGGAGTCTGCTATTCCCTGCCGGTTACGTCA 180
Db 180 CCCGAAATTTATACATGACTGAAAGGAGGAGTCTGCTATTCCCTGCCGGTTACGTCA 239
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Qy 361 CATCGACAAACCAATCAATCATAGATGTGGTCTGAGTCCGTCCTCATGGAAATTTGAACATA 420
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Db 540 GACTTCAACTGGGAAATACCTTCTTCCGAAGCATCAGCATAGAACTTGTAAACCGAGAC 599
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Db 660 GTAAACCCGGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 719
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Qy	661	AAGAAGCAGCATTTGT	CAGGTCCATGAAAG-----GACAAA	CTCACATGC	711
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Db	780	CCACCGTCCCGAGC	ACCTGAACTCCTGGGGGACCGT	CAGTCTTCTCTTCCCCCAAAA	839
Qy	772	CCAAAGGACACCTCAT	GTATCTCCCGGACCCCTGAGGT	CACATGCGTGGTGGGACGTG	831
Db	840	CCAAAGGACACCTCAT	GTATCTCCCGGACCCCTGAGGT	CACATGCGTGGTGGGACGTG	899
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Qy	892	GCCAAAGACAAAGCC	CGGGAGGAGCAGTACAACAGCACGT	ACCGTGTGGTCAAGCTCCTC	951
Db	960	GCCAAAGACAAAGCC	CGGGAGGAGCAGTACAACAGCACGT	ACCGTGTGGTCAAGCTCCTC	1019
Qy	952	ACCGTCTGTGAC	CACGAGTGGCTGAATGGCAAGGAGT	ACAAGTGCAGGTCTCCAAACAA	1011
Db	1020	ACCGTCTGTGAC	CACGAGTGGCTGAATGGCAAGGAGT	ACAAGTGCAGGTCTCCAAACAA	1079
Qy	1012	GCCCTCCAGCC	CCCATCGAGAAAACCATCTCCAAAGCC	AAAGGGCAGCCCCGAGAACCA	1071
Db	1080	GCCCTCCAGCC	CCCATCGAGAAAACCATCTCCAAAGCC	AAAGGGCAGCCCCGAGAACCA	1139
Qy	1072	CAGGTGTACAC	CCCTGCCCCCATCCCGGATGAGT	GACCAAGAACCAAGGTCAAGCTGACC	1131
Db	1140	CAGGTGTACAC	CCCTGCCCCCATCCCGGATGAGT	GACCAAGAACCAAGGTCAAGCTGACC	1199
Qy	1132	TGCTGTGTC	AAAGGCTTCTATCCAGCGACAT	CGCGTGGAGTGGGAGAGCAATGGGCGAG	1191
Db	1200	TGCTGTGTC	AAAGGCTTCTATCCAGCGACAT	CGCGTGGAGTGGGAGAGCAATGGGCGAG	1259
Qy	1192	CCGAGAACAACT	ACAAGACACGCTCCCGTGTGACT	CCGACGGCTCCTTCTTCCTC	1251
Db	1260	CCGAGAACAACT	ACAAGACACGCTCCCGTGTGACT	CCGACGGCTCCTTCTTCCTC	1319
Qy	1252	TACAGCAAGT	TCACCGTGGACAAGAGCAGGT	GGCAGCGGGAACGTCTTCTCATGCTCC	1311
Db	1320	TATAGCAAGT	TCACCGTGGACAAGAGCAGGT	GGCAGCGGGAACGTCTTCTCATGCTCC	1379
Qy	1312	GTGATGAT	GAGGCTCTGCAAAACCACTACA	CGCAGAAAGCCCTCTCCCTGTCTCCGGGT	1371
Db	1380	GTGATGAT	GAGGCTCTGCAAAACCACTACA	CGCAGAAAGCCCTCTCCCTGTCTCCGGGT	1439
Qy	1372	AAATGA	1377		
Db	1440	AAATGA	1445		

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Job time : 937 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 23, 2005, 15:40:31 ; Search time 120 seconds  
(without alignments)  
1954.436 Million cell updates/sec

Title: US-10-811-170-2

Perfect score: 2437

Sequence: 1 MVSYDVTGVLCCALLSCLLL.....MHEALHHYTKSLSPGK 458

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Uniprot\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1267.5	52.0	466	2	Q6IN78	Q6IN78 homo sapien
2	1253.5	51.4	487	2	Q65ZL2	Q65ZL2 mus sp. fv/
3	1252.5	51.4	472	2	Q6N089	Q6N089 homo sapien
4	1252	51.4	470	2	Q6PJ44	Q6PJ44 homo sapien
5	1246.5	51.1	475	2	Q6MZQ6	Q6MZQ6 homo sapien
6	1246	51.1	478	2	Q6P181	Q6P181 homo sapien
7	1245.5	51.1	465	2	Q6GMX6	Q6GMX6 homo sapien
8	1245	51.1	476	2	Q6GMX1	Q6GMX1 homo sapien
9	1244.5	51.1	475	2	Q6GMW7	Q6GMW7 homo sapien
10	1242.5	51.0	482	2	Q7Z351	Q7Z351 homo sapien
11	1240.5	50.9	330	1	GC1_HUMAN	P01857 homo sapien
12	1240.5	50.9	469	2	Q7Z7P5	Q7Z7P5 homo sapien
13	1240.5	50.9	470	2	Q7Z5W1	Q7Z5W1 homo sapien
14	1239.5	50.9	473	2	Q6MZV7	Q6MZV7 homo sapien
15	1237.5	50.8	348	2	Q6PYX1	Q6PYX1 homo sapien
16	1237.5	50.8	480	2	Q6PJF1	Q6PJF1 homo sapien
17	1236.5	50.7	473	2	Q6P055	Q6P055 homo sapien
18	1236.5	50.7	480	2	Q6N094	Q6N094 homo sapien
19	1236.5	50.7	481	2	Q6N097	Q6N097 homo sapien
20	1235	50.7	466	2	Q6N096	Q6N096 homo sapien
21	1233	50.6	679	2	Q96PQ8	Q96PQ8 homo sapien
22	1229.5	50.5	475	2	Q6N095	Q6N095 homo sapien
23	1229.5	50.5	544	2	Q6P095	Q6P095 homo sapien
24	1155	47.4	464	2	Q6MZU6	Q6MZU6 homo sapien
25	1150	47.2	417	2	Q6N093	Q6N093 homo sapien
26	1149.5	47.2	518	2	Q6N030	Q6N030 homo sapien
27	1148.5	47.1	326	1	GC2_HUMAN	P01859 homo sapien
28	1146.5	47.0	465	2	Q6P6C4	Q6P6C4 homo sapien
29	1146	46.9	354	2	Q86TT2	Q86TT2 homo sapien
30	1144	46.9	327	1	GC4_HUMAN	P01861 homo sapien
31	1144	46.9	473	2	Q8TC63	Q8TC63 homo sapien

32	1142	46.9	521	2	Q8N4Y9	Q8N4Y9 homo sapien
33	1135	46.6	476	2	Q6MZX7	Q6MZX7 homo sapien
34	1134.5	46.6	493	2	Q68CN4	Q68CN4 homo sapien
35	1131	46.4	509	2	Q8NF17	Q8NF17 homo sapien
36	1126	46.2	290	1	GC3_HUMAN	P01860 homo sapien
37	925.5	38.0	323	1	GC_RABIT	P01870 oryctolagus
38	917	37.6	337	2	Q95M34	Q95M34 equus caball
39	900	36.9	329	1	GC2_CAVPO	P01862 cavia porce
40	872	35.8	470	2	Q7TMK1	Q7TMK1 mus musculus
41	866.5	35.6	329	1	GC3_MOUSE	P22436 mus musculus
42	855.5	35.1	398	1	GC3M_MOUSE	P03987 mus musculus
43	854	35.0	464	2	Q6PIF8	Q6PIF8 mus musculus
44	851	34.9	458	2	Q65ZQ1	Q65ZQ1 homo sapien
45	847.5	34.8	463	2	Q991C4	Q991C4 mus musculus

#### ALIGNMENTS

RESULT 1

Q6IN78 PRELIMINARY; PRT; 466 AA.

AC Q6IN78; (Tremblrel. 27, Created)

DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)

DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)

DE IGHG1 protein.

GN Name=IGHG1;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Peripheral Nervous System;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;

RA "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Peripheral Nervous System;

RA Strausberg R.;

RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC072419; AAH72419.1; -.

DR HSSP; P01861; IADO.

DR InterPro; IPR003599; IG.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003597; IG.cl.

DR InterPro; IPR003006; IG.MHC.

DR InterPro; IPR003596; IG.v.

DR Pfam; PF07654; C1-set; 3.

DR SMART; SM00409; IG; 2.

DR SMART; SM00407; IGcl; 3.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG\_LIKE; 4.





DR PROSITE; PS00290; IG MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 51.4%; Score 1252.5; DB 2; Length 472;  
Best Local Similarity 59.1%; Pred. No. 9.3e-79;  
Matches 273; Conservative 24; Mismatches 90; Indels 75; Gaps 14;

Qy 49 GRELVIPCRVTSNPIITVTLKKFPDITLI-----PDGKRRIIW-----DSRK 88  
Db 34 GRSRLSCAASG-----FTDDYAMHWVRQAPGKLEWVSGISWNSSGIAYADSVK 84

Qy 89 G-FIIS-----NATYKEIGLLTCAATV-----NGHLYKTNLYTHRQTNIIDV- 130  
Db 85 GRFTISRDNKNSLYLQWNSLRADETALYCAKEIGAHNFYFYGMVDMGQGTITVTSSAS 144

Qy 131 -----VLSPSHGIELSVGEKLVNCTARTELNVGIDFNWE---YPSKSHQHKLVNRD 180  
Db 145 TKGSVFPPLAPSS--KSTSGGTAALGCLVVDYFPEPVTVSWNSGALTSGVHTFFPAVL--- 199

Qy 181 LKTSQSGEMKFLSTLTIDGVTRSDQGLYTCAASSGLMKNSTFV--RVHEK--DKTHT 236  
Db 200 ----QSSGLYSLSSVTVTPSSSLGTO--TYICNVNH-----KPSNTKVDKVEPKSCDKTHT 250

Qy 237 CPPCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 296  
Db 251 CPPCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 310

Qy 297 NAKTKPREEQNSTYRVVSVLTVLHODWLNKGEVKCKVSNKALPAPIEKTISKAKGQPRE 356  
Db 311 NAKTKPREEQNSTYRVVSVLTVLHODWLNKGEVKCKVSNKALPAPIEKTISKAKGQPRE 370

Qy 357 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYTKTTPVLDSDGSFF 416  
Db 371 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYTKTTPVLDSDGSFF 430

Qy 417 LYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPGK 458  
Db 431 LYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPGK 472

RESULT 4  
Q6PUA4  
ID Q6PUA4 PRELIMINARY; PRT; 470 AA.  
AC Q6PUA4;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Berge J.G.,  
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,  
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
Rosa S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;  
"Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;  
RA Strausberg R.;  
SUBMITTED (DSC-2001) to the EMBL/GenBank/DBJ databases.  
RL EMBL; BC018747; AAH18747.1; --  
DR HSP; P01861; IADQ.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG cl.  
DR InterPro; IPR003006; IG MHC.  
DR InterPro; IPR003596; IG v.  
DR Pfam; PF07654; Cl-bet; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IG1; 3.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS00835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 470 AA; 51715 MW; 7B49556A11FD7D99 CRC64;

Query Match 51.4%; Score 1252; DB 2; Length 470;  
Best Local Similarity 62.4%; Pred. No. 1e-78;  
Matches 262; Conservative 23; Mismatches 85; Indels 50; Gaps 9;

Qy 79 GKRIIW-----DSRKG-FIIS-----NATYKEIGLLTCAATV-----NGH 112  
Db 61 GKGLEWVANIKQDGSEKYYVDSVKGRFTISRDNKNSLYLQWNSLRADETAVYVCARDGS 120

Qy 113 LYKTNLYTHRQTNIIDV-----VLSPSHGIELSVGEKLVNCTARTELNVGID 161  
Db 121 SWYRDFWDPNGQGLTVTVSSASTKGPSPVFLAPSS--KSTSGGTAALGCLVKDYFPEPVT 178

Qy 162 FNWE---YPSKSHQHKLVNRDLTKQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLM 218  
Db 179 VSWNSGALTSGVHTFFPAVL-----QSSGLYSLSSVTVTPSSSLGTO--TYICNVNHPKS 230

Qy 219 TKKNSTFVRVHEKDKTHTCCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVS 278  
Db 231 NTKVDKVKVEPKSCDKTHTCCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVS 290

Qy 279 HEDPEVKFNWYVDGVEVHNAKTKEPREEQNSTYRVVSVLTVLHODWLNKGEVKCKVSNKA 338  
Db 291 HEDPEVKFNWYVDGVEVHNAKTKEPREEQNSTYRVVSVLTVLHODWLNKGEVKCKVSNKA 350

Qy 339 LPAPIEKTISKAKGQPREPOVYITLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP 398  
Db 351 LPAPIEKTISKAKGQPREPOVYITLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP 410

Qy 399 ENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPGK 458  
Db 411 ENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPGK 470

RESULT 5  
Q6MZQ6  
ID Q6MZQ6 PRELIMINARY; PRT; 475 AA.  
AC Q6MZQ6;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein DKFZp686G11190.  
GN Name=DKFZp686G11190;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.









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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----  
DR EMBL; J00228; AAC82527.1; ALT\_INIT.  
DR PIR; A93433; GHU.  
DR PDB; 1A07; X-ray; H=1-103.  
DR PDB; 1D5B; X-ray; B/H=1-101.  
DR PDB; 1D51; X-ray; H=1-101.  
DR PDB; 1D6V; X-ray; H=1-101.  
DR PDB; 1DN2; X-ray; A/B=120-326.  
DR PDB; 1E4K; X-ray; A/B=106-329.  
DR PDB; 1FCL; X-ray; A/B=106-329.  
DR PDB; 1FC2; X-ray; D=106-329.  
DR PDB; 1FCC; X-ray; A=121-326.  
DR PDB; 1H2H; X-ray; H/K=1-330.  
DR PDB; 1I7Z; X-ray; B/D=1-103.  
DR PDB; 1IIS; X-ray; A/B=107-330.  
DR PDB; 1IIX; X-ray; A/B=107-330.  
DR PDB; 1L6X; X-ray; A=120-326.  
DR PDB; 1LQX; X-ray; A/B=119-330.  
DR PDB; 2RGS; X-ray; H=1-103.  
DR Genew; HGNC:5525; IGHG1.  
DR MIM; 147100; .  
DR GO; GO:0005624; C:membrane fraction; NAS.  
DR GO; GO:0003823; F:antigen binding; TAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF00047; ig; 3.  
DR PROSITE; PS00835; IG\_LIKE; 3.  
DR PROSITE; PS00290; IG\_MHC; 2.  
DR 3D-structure; Direct protein sequencing; Glycoprotein;  
KW Immunoglobulin C region; Immunoglobulin domain.  
FT NON\_TER 1 1  
FT DOMAIN 1 98 CH1.  
FT DOMAIN 99 110 Hinge.  
FT DOMAIN 111 223 CH2.  
FT DOMAIN 224 330 CH3.  
FT DISULFID 27 83 Interchain (with light chain).  
FT DISULFID 103 103 Interchain (with heavy chain).  
FT DISULFID 109 109 Interchain (with heavy chain).  
FT DISULFID 112 112 Interchain (with heavy chain).  
FT DISULFID 144 204 N-linked (GLCNAC...).  
FT DISULFID 250 308 K -> R (in GIM(3) marker).  
FT CARBOHYD 180 180 /FTId=VAR\_003886.  
FT VARIANT 97 97 D -> E (in GIM(non-1) marker).  
FT VARIANT 239 239 /FTId=VAR\_003887.  
FT VARIANT 241 241 L -> M (in GIM(non-1) marker).  
FT STRAND 23 24 /FTId=VAR\_003888.  
FT STRAND 26 33  
FT STRAND 38 38  
FT STRAND 41 41  
FT TURN 42 45  
FT TURN 48 49  
FT STRAND 50 52  
FT STRAND 57 58  
FT TURN 59 61  
FT STRAND 62 71  
FT HELIX 73 75  
FT TURN 76 78  
FT STRAND 82 87  
FT TURN 88 91  
FT STRAND 92 97  
FT TURN 102 103  
FT STRAND 122 126  
FT HELIX 130 134  
FT TURN 136 137  
FT STRAND 141 149

FT STRAND 157 162  
FT TURN 163 164  
FT STRAND 165 167  
FT STRAND 171 172  
FT STRAND 176 177  
FT TURN 179 180  
FT STRAND 183 190  
FT HELIX 193 197  
FT TURN 198 199  
FT STRAND 202 207  
FT TURN 209 210  
FT STRAND 215 219  
FT STRAND 227 227  
FT STRAND 230 234  
FT HELIX 238 242  
FT STRAND 245 256  
FT STRAND 261 266  
FT TURN 267 268  
FT STRAND 269 270  
FT STRAND 274 276  
FT STRAND 280 281  
FT TURN 283 284  
FT STRAND 287 296  
FT HELIX 297 301  
FT TURN 302 303  
FT STRAND 306 311  
FT TURN 313 314  
FT HELIX 316 318  
FT STRAND 319 324  
SQ SEQUENCE 330 AA; 36106 MW; 3770EE106C2FA33D CRC64;  
  
Query Match 50.9%; Score 1240.5; DB 1; Length 330;  
Best Local Similarity 86.4%; Pred. No. 4e-78;  
Matches 242; Conservative 7; Mismatches 12; Indels 19; Gaps 5;  
  
QY 197 TIDGTRSDQGLYTCAA-----SSGLMT-----KKNSTFV--RVHEK--DKTHTCP 238  
Db 52 TTPAVLQS--SGLYSLSSVVTVFSSSLGTQTYICNNHKFSNTKVKVFPKSCDKTHTCP 110  
  
QY 239 PCPAPELLGGPSVFLFPPPKKDTLMISRTPEVTVVVDVSHEDPEVKFNWYVDGVEVHNA 298  
Db 111 PCPAPELLGGPSVFLFPPPKKDTLMISRTPEVTVVVDVSHEDPEVKFNWYVDGVEVHNA 170  
  
QY 299 KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 358  
Db 171 KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 230  
  
QY 359 VYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLY 418  
Db 231 VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLY 290  
  
QY 419 SKLTVDKSRWQQGNVPCSVMEALHNHYTQKSLSLSPGK 458  
Db 291 SKLTVDKSRWQQGNVPCSVMEALHNHYTQKSLSLSPGK 330  
  
RESULT 12  
Q7Z7P5 PRELIMINARY; PRT; 469 AA.  
ID Q7Z7P5  
AC Q7Z7P5; (TREMELrel. 25, Created)  
DT 01-OCT-2003 (TREMELrel. 25, Last sequence update)  
DT 01-OCT-2003 (TREMELrel. 25, Last sequence update)  
DE 01-MAR-2004 (TREMELrel. 26, Last annotation update)  
DE IGHG1 protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Pahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RA Strausberg R.;  
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC051328; AAH51328.1; -;  
DR HSSP; P01857; 1H2H.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; Cl-set; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
SQ SEQUENCE 469 AA; 51395 MW; C8DBBE12BAAF795C CRC64;

Query Match 50.9%; Score 1240.5; DB 2; Length 469;  
Best Local Similarity 86.4%; Pred. No. 6.3e-78;  
Matches 242; Conservative 7; Mismatches 12; Indels 19; Gaps 5;  
QY 197 TIDGVTFRSDGLYTCAA-----SSGLMT-----KKNSTFV--RVHEK--DKHTTCTP 238  
Db 191 TTPAVLQSGSLYSLSSVVTVPSSSLGTQTYICNVNHPKPSNTKVDKKEPKSCDKHTTCTP 249  
QY 239 PCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 298  
Db 250 PCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 309  
QY 299 KTKPREEQNSTYRVVSVLTVLHQDLNGLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQ 358  
Db 310 KTKPREEQNSTYRVVSVLTVLHQDLNGLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQ 369  
QY 359 VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLY 418  
Db 370 VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLY 429  
QY 419 SKLTVDKSRWQOGNVFSCSVMHREALNHYTKLSLSPGK 458  
Db 430 SKLTVDKSRWQOGNVFSCSVMHREALNHYTKLSLSPGK 469

RESULT 13  
Q725W1  
ID Q725W1 PRELIMINARY; PRT; 470 AA.  
AC Q725W1;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;

RN SEQUENCE FROM N.A.  
RP TISSUE=Spleen;  
RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Pahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RA Strausberg R.;  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC053984; AAH53984.1; -;  
DR HSSP; P01857; 1H2H.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; Cl-set; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;

Query Match 50.9%; Score 1240.5; DB 2; Length 470;  
Best Local Similarity 86.4%; Pred. No. 6.3e-78;  
Matches 242; Conservative 7; Mismatches 12; Indels 19; Gaps 5;  
QY 197 TIDGVTFRSDGLYTCAA-----SSGLMT-----KKNSTFV--RVHEK--DKHTTCTP 238  
Db 192 TTPAVLQSGSLYSLSSVVTVPSSSLGTQTYICNVNHPKPSNTKVDKKEPKSCDKHTTCTP 250  
QY 239 PCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 298  
Db 251 PCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 310  
QY 299 KTKPREEQNSTYRVVSVLTVLHQDLNGLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQ 358  
Db 311 KTKPREEQNSTYRVVSVLTVLHQDLNGLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQ 370  
QY 359 VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLY 418  
Db 371 VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLY 430  
QY 419 SKLTVDKSRWQOGNVFSCSVMHREALNHYTKLSLSPGK 458  
Db 431 SKLTVDKSRWQOGNVFSCSVMHREALNHYTKLSLSPGK 470

RESULT 14  
Q6MZV7  
ID Q6MZV7 PRELIMINARY; PRT; 473 AA.  
AC Q6MZV7;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 23, 2005, 14:00:46 ; Search time 120 Seconds  
(without alignments)  
1476.135 Million cell updates/sec

Title: US-10-811-170-2

Perfect score: 2437

Sequence: 1 MVSYDVTGVLLCALLSCLLL.....MHEALHNYTKSLSLSPGK 458

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: Genesecp1980s:\*
- 2: Genesecp1990s:\*
- 3: Genesecp2000s:\*
- 4: Genesecp2001s:\*
- 5: Genesecp2002s:\*
- 6: Genesecp2003as:\*
- 7: Genesecp2003bs:\*
- 8: Genesecp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2437	100.0	458	4 AAY97596	Aay97596 Flt1 rece
2	2437	100.0	458	5 ABP52449	Abp52449 Modified
3	2399	98.4	458	4 AAY97594	Aay97594 Flt1 rece
4	2399	98.4	458	5 ABP52447	Abp52447 Modified
5	2275.5	93.4	432	5 AAY975450	Aay975450 Flt1D2.Fl
6	2069.5	84.9	455	4 AAY97595	Aay97595 Flt1 rece
7	2069.5	84.9	455	5 ABP52448	Abp52448 Modified
8	2049	84.1	462	4 AAY97592	Aay97592 Flt1 rece
9	2049	84.1	462	5 ABP52445	Abp52445 Mutation
10	2038	83.6	452	4 AAY97591	Aay97591 Flt1 rece
11	2038	83.6	452	5 ABP52444	Abp52444 Mutation
12	2015.5	82.7	567	4 AAY97593	Aay97593 Flt1 rece
13	2015.5	82.7	567	5 ABP52446	Abp52446 Mutation
14	2014.5	82.7	567	4 AAY97597	Aay97597 Flt1 rece
15	2014.5	82.7	567	5 ABP52442	Abp52442 Flt1(1-3)
16	2003.5	82.2	557	4 AAY97590	Aay97590 Flt1 rece
17	2003.5	82.2	557	5 ABP52443	Abp52443 Mutation
18	1726.5	70.8	934	6 ABP70840	Abp70840 WVP-B pro
19	1716	70.4	949	6 ABP70841	Abp70841 WVP-C pro
20	1627.5	66.8	816	6 ABP70853	Abp70853 WVP-A pro
21	1619.5	66.5	810	6 ABP70839	Abp70839 WVP-A pro
22	1304	53.5	680	2 AAR48037	Aar48037 tICAM(453
23	1304	53.5	680	2 ABU07273	Abu07273 Human exp
24	1293.5	53.1	915	7 ABW02188	Abw02188 Human IL-
25	1292	53.0	640	8 ADP76035	Adp76035 AMIGO pol

#### ALIGNMENTS

RESULT 1

AAY97596  
ID AAY97596 standard; protein; 458 AA.

XX  
AC AAY97596;

XX  
DT 05-APR-2001 (first entry)

XX  
DE Flt1 receptor fusion protein VEGFR1R2-FcDeltaC1(a).

XX  
KW Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic;

XX  
KW plasma leakage; vascular permeability; IGG Fc region.

XX  
OS Unidentified.

XX  
PN WO200075319-A1.

XX  
PD 14-DEC-2000.

XX  
PF 23-MAY-2000; 2000WO-US014142.

XX  
PR 08-JUN-1999; 99US-0138133P.

XX  
(REGE-) REGENERON PHARM INC.

XX  
Papadopoulos NJ, Davis S, Yancopoulos GD;

XX  
WPI; 2001-071076/08.

XX  
N-PSDB; AAA91076.

XX  
PT Nucleic acid molecule encoding mammalian phospholipid transfer protein, and its fragments, useful for diagnosis, evaluation, and treatment of diseases associated with the gene expression and for producing model systems.

XX  
Claim 49; Fig 24; 159pp; English.

XX  
CC This sequence represents a fusion protein of the invention between the Flt1 receptor and the Fc region of IGG. The specification relates to modified chimeric polypeptides with improved pharmacokinetics. The modified chimeric polypeptides are preferably Flt1 receptor polypeptides that have been modified to improve their pharmacokinetic profile. The polypeptides can be used to decrease or inhibit plasma leakage and/or vascular permeability in a mammal

XX  
SQ Sequence 458 AA;

Query Match 100.0%; Score 2437; DB 4; Length 458;

Best Local Similarity 100.0%; Pred. No. 1.1e-153; Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 1 MVS YWDTGVLLCALLSCLLTGSSGSDTGRPFVEMYSEIPIIHMTEGRELVIPCRVTS 60	PT administration of a vascular endothelial cell growth factor (VEGF)
DB 1 MVS YWDTGVLLCALLSCLLTGSSGSDTGRPFVEMYSEIPIIHMTEGRELVIPCRVTS 60	PT antagonist.
QY 61 PNI TVTLKKFPDLTLIPDGKRIIWSRKGFIIISNATYKEIGLLTCEATVNGHLYKTNLYT 120	XX Example 20; Fig 24A-C; 179pp; English.
DB 61 PNI TVTLKKFPDLTLIPDGKRIIWSRKGFIIISNATYKEIGLLTCEATVNGHLYKTNLYT 120	XX The present invention describes a method for treating psoriasis and enhancing wound healing in a mammal or a human. The method comprises administering a vascular endothelial cell growth factor (VEGF) antagonist to the mammal or human. A VEGF antagonist has anti-psoriatic, anti-inflammatory, vulnerary, antiasthmatic, anti-rheumatic, antiarthritic, nephrotropic and ophthalmological activities. The method can be used in treating psoriasis and enhancing wound healing in humans by administering VEGF antagonist. The method is also useful in treating clinical conditions characterised by vascular permeability, oedema or inflammation, such as brain oedema associated with injury, oedema associated with inflammatory disorders (e.g. rheumatoid arthritis), asthma, burns, kidney diseases, or eye disorders such as age-related macular degeneration and diabetic retinopathy. The method may also be used in making the polypeptide to decrease or inhibit plasma leakage and or vascular permeability. The present sequence represents VEGFR1R2-CC FcDELTA1(a) which is used in an example from the present invention
QY 121 HRQTNTIIDVLSPSHGIELSVGEKLVNCTARTELNVGIDFNWEYPSKHOHKKLVNRD 180	CC VEGF antagonist.
DB 121 HRQTNTIIDVLSPSHGIELSVGEKLVNCTARTELNVGIDFNWEYPSKHOHKKLVNRD 180	CC conditions characterised by vascular permeability, oedema or inflammation, such as brain oedema associated with injury, oedema associated with inflammatory disorders (e.g. rheumatoid arthritis), asthma, burns, kidney diseases, or eye disorders such as age-related macular degeneration and diabetic retinopathy. The method may also be used in making the polypeptide to decrease or inhibit plasma leakage and or vascular permeability. The present sequence represents VEGFR1R2-CC FcDELTA1(a) which is used in an example from the present invention
QY 181 LKTSQSEMKKFLSTLTIDGVTSDQGLYTCAASSGLMTKKNSTFVRVHEKDKTHTCPPC 240	CC VEGF antagonist.
DB 181 LKTSQSEMKKFLSTLTIDGVTSDQGLYTCAASSGLMTKKNSTFVRVHEKDKTHTCPPC 240	CC conditions characterised by vascular permeability, oedema or inflammation, such as brain oedema associated with injury, oedema associated with inflammatory disorders (e.g. rheumatoid arthritis), asthma, burns, kidney diseases, or eye disorders such as age-related macular degeneration and diabetic retinopathy. The method may also be used in making the polypeptide to decrease or inhibit plasma leakage and or vascular permeability. The present sequence represents VEGFR1R2-CC FcDELTA1(a) which is used in an example from the present invention
QY 241 PAPELLGGPSVFLFPKPKDTLMI SRTPEVTCVVDVSHEDPEVKFNWYDGVVEVHNAKT 300	CC VEGF antagonist.
DB 241 PAPELLGGPSVFLFPKPKDTLMI SRTPEVTCVVDVSHEDPEVKFNWYDGVVEVHNAKT 300	CC conditions characterised by vascular permeability, oedema or inflammation, such as brain oedema associated with injury, oedema associated with inflammatory disorders (e.g. rheumatoid arthritis), asthma, burns, kidney diseases, or eye disorders such as age-related macular degeneration and diabetic retinopathy. The method may also be used in making the polypeptide to decrease or inhibit plasma leakage and or vascular permeability. The present sequence represents VEGFR1R2-CC FcDELTA1(a) which is used in an example from the present invention
QY 301 KPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVY 360	CC VEGF antagonist.
DB 301 KPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVY 360	CC conditions characterised by vascular permeability, oedema or inflammation, such as brain oedema associated with injury, oedema associated with inflammatory disorders (e.g. rheumatoid arthritis), asthma, burns, kidney diseases, or eye disorders such as age-related macular degeneration and diabetic retinopathy. The method may also be used in making the polypeptide to decrease or inhibit plasma leakage and or vascular permeability. The present sequence represents VEGFR1R2-CC FcDELTA1(a) which is used in an example from the present invention
QY 361 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFPLYSK 420	CC VEGF antagonist.
DB 361 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFPLYSK 420	CC conditions characterised by vascular permeability, oedema or inflammation, such as brain oedema associated with injury, oedema associated with inflammatory disorders (e.g. rheumatoid arthritis), asthma, burns, kidney diseases, or eye disorders such as age-related macular degeneration and diabetic retinopathy. The method may also be used in making the polypeptide to decrease or inhibit plasma leakage and or vascular permeability. The present sequence represents VEGFR1R2-CC FcDELTA1(a) which is used in an example from the present invention
QY 421 LTVDKSRWQOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 458	QY Query Match 100.0%; Score 2437; DB 5; Length 458; Best Local Similarity 100.0%; Pred. No. 1.1e-153; Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 421 LTVDKSRWQOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 458	DB 1 MVS YWDTGVLLCALLSCLLTGSSGSDTGRPFVEMYSEIPIIHMTEGRELVIPCRVTS 60
RESULT 2	DB 1 MVS YWDTGVLLCALLSCLLTGSSGSDTGRPFVEMYSEIPIIHMTEGRELVIPCRVTS 60
ABP52449	QY 61 PNI TVTLKKFPDLTLIPDGKRIIWSRKGFIIISNATYKEIGLLTCEATVNGHLYKTNLYT 120
ID ABP52449 standard; protein; 458 AA.	DB 61 PNI TVTLKKFPDLTLIPDGKRIIWSRKGFIIISNATYKEIGLLTCEATVNGHLYKTNLYT 120
XX	QY 121 HRQTNTIIDVLSPSHGIELSVGEKLVNCTARTELNVGIDFNWEYPSKHOHKKLVNRD 180
AC ABP52449;	DB 121 HRQTNTIIDVLSPSHGIELSVGEKLVNCTARTELNVGIDFNWEYPSKHOHKKLVNRD 180
DT 23-OCT-2002 (first entry)	QY 181 LKTSQSEMKKFLSTLTIDGVTSDQGLYTCAASSGLMTKKNSTFVRVHEKDKTHTCPPC 240
DE Modified Flt1 receptor VEGFR1R2-FcDELTA1(a) protein sequence.	DB 181 LKTSQSEMKKFLSTLTIDGVTSDQGLYTCAASSGLMTKKNSTFVRVHEKDKTHTCPPC 240
XX	QY 241 PAPELLGGPSVFLFPKPKDTLMI SRTPEVTCVVDVSHEDPEVKFNWYDGVVEVHNAKT 300
KW Human; Flt1; vascular endothelial growth factor; VEGF; VEGF antagonist; psoriasis; wound healing; Flt1 receptor; anti-psoriatic; anti-inflammatory; vulnerary; antiasthmatic; anti-rheumatic; antiarthritic; nephrotropic; ophthalmological; vascular permeability; oedema; inflammation; asthma; brain oedema; inflammatory disorder; rheumatoid arthritis; burn; kidney disease; eye disorder; age-related macular degeneration; diabetic retinopathy.	DB 241 PAPELLGGPSVFLFPKPKDTLMI SRTPEVTCVVDVSHEDPEVKFNWYDGVVEVHNAKT 300
XX	QY 301 KPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVY 360
OS Homo sapiens.	DB 301 KPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVY 360
OS Synthetic.	QY 361 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFPLYSK 420
PN WO200260489-A1.	DB 361 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFPLYSK 420
PD 08-AUG-2002.	QY 421 LTVDKSRWQOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 458
PF 28-JAN-2002; 2002WO-US002466.	DB 421 LTVDKSRWQOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 458
XX	RESULT 3
XX	AAAY97594
PR 31-JAN-2001; 2001US-00773877.	ID AAAY97594 standard; protein; 458 AA.
XX	XX
PA (REG- ) REGENERON PHARM INC.	XX AAAY97594;
XX	DT 05-APR-2001 (first entry)
PI Xia Y, Rudge JS, Yancopoulos GD;	XX
XX	DE Flt1 receptor fusion protein Flt1b2.Flk1D3.FcDelta1(a).
DR WPI; 2002-608488/65.	XX
DR N-PSDB; ABQ74610.	KW Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic; plasma leakage; vascular permeability; IgG Fc region.
PT	KW



```

Qy 121 HROQNTIIDVVLSPSHGIELSVGKLVNCTARTELNVGIDFNWEYPSSKHQHKLVNRD 180
Db 118 HROQNTIIDVVLSPSHGIELSVGKLVNCTARTELNVGIDFNWEYPSSKHQHKLVNRD 177
Qy 181 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCASSGLMTKKNSTFVRVHEK---DKTHTC 237
Db 178 LKTQSGSEMKKFLSTLTIDGVTRSDQGLYTCASSGLMTKKNSTFVRVHEKPGDKTHTC 237
Qy 238 PPCAPELGGPSVFLPPPKDITMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHN 297
Db 238 PPCAPELGGPSVFLPPPKDITMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHN 297
Qy 298 AKTPREEQNSTYRVVSVLTVLHQDLNMGKEYCKVSNKALPAPIETISKAKGQPREP 357
Db 298 AKTPREEQNSTYRVVSVLTVLHQDLNMGKEYCKVSNKALPAPIETISKAKGQPREP 357
Qy 358 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFL 417
Db 358 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFL 417
Qy 418 YSKLTVDKSRWQGNVFSCSVHREALNHYTKQSLSLSPGK 458
Db 418 YSKLTVDKSRWQGNVFSCSVHREALNHYTKQSLSLSPGK 458

RESULT 5
ID ABP52450 standard; protein; 432 AA.
AC ABP52450;
XX
XX
DT 23-OCT-2002 (first entry)
DE
DE
XX Human; Flt1; vascular endothelial growth factor; VEGF; VEGF antagonist;
KW psoriasis; wound healing; Flt1 receptor; antiapoptotic; antiinflammatory;
KW vulnary; antiasthmatic; antirheumatic; antiarthritic; nephrotropic;
KW ophthalmological; vascular permeability; oedema; inflammation; asthma;
KW brain oedema; inflammatory disorder; rheumatoid arthritis; burn;
KW kidney disease; eye disorder; age-related macular degeneration;
KW diabetic retinopathy.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Disulfide-bond 27..76
FT Disulfide-bond 121..182
FT Disulfide-bond 246..306
FT Disulfide-bond 352..410
XX
XX WO200260489-A1.
XX
XX 08-AUG-2002.
XX
XX 28-JAN-2002; 2002WO-US002466.
XX
XX 31-JAN-2001; 2001US-00773877.
XX
XX (REG- ) REGENERON PHARM INC.
XX
XX Xia Y, Rudge JS, Yancopoulos GD;
XX WPI; 2002-608488/65.
XX
XX Treating psoriasis and enhancing wound healing in humans comprises the
XX administration of a vascular endothelial cell growth factor (VEGF)
XX antagonist.
XX
XX Example 28; Fig 36; 179pp; English.
XX
XX The present invention describes a method for treating psoriasis and

```

```

CC enhancing wound healing in a mammal or a human. The method comprises
CC administering a vascular endothelial cell growth factor (VEGF) antagonist
CC to the mammal or human. A VEGF antagonist has antiapoptotic,
CC antiinflammatory, vulnary, antiasthmatic, antirheumatic, antiarthritic,
CC nephrotropic and ophthalmological activities. The method can be used in
CC treating psoriasis and enhancing wound healing in humans by administering
CC VEGF antagonist. The method is also useful in treating clinical
CC conditions characterised by vascular permeability, oedema or
CC inflammation, such as brain oedema associated with injury, oedema
CC associated with inflammatory disorders (e.g. rheumatoid arthritis),
CC asthma, burns, kidney diseases, or eye disorders such as age-related
CC macular degeneration and diabetic retinopathy. The method may also be
CC used in making the polypeptide to decrease or inhibit plasma leakage and
CC or vascular permeability. The present sequence represents
CC Flt1D2.Flt1D3.FcDELTA1(a) which is used in an example from the present
CC invention
XX
XX SQ Sequence 432 AA;
XX
XX Query Match 93.4%; Score 2275.5; DB 5; Length 432;
XX Best Local Similarity 99.3%; Pred. No. 5.8e-143;
XX Matches 429; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
XX
Qy 30 GRPFVEMYSEIPIIHMTEGRELVIKRVTSPTNITVTLKKFPLDTLPDGKRIIWDNRKG 89
Db 1 GRPFVEMYSEIPIIHMTEGRELVIKRVTSPTNITVTLKKFPLDTLPDGKRIIWDNRKG 60
Qy 90 FIISNATYKEIGLLTCEATVNGHLYKTNLYTHRQTNTIIDVLSPSHGIELSVGEKLVN 149
Db 61 FIISNATYKEIGLLTCEATVNGHLYKTNLYTHRQTNTIIDVLSPSHGIELSVGEKLVN 120
Qy 150 CTARTELNVGIDFNWEYPSSKHQHKLVNRDLTKQSGSEMKKFLSTLTIDGVTRSDQGLY 209
Db 121 CTARTELNVGIDFNWEYPSSKHQHKLVNRDLTKQSGSEMKKFLSTLTIDGVTRSDQGLY 180
Qy 210 TCAASSGLMTKKNSTFVRVHEK---DKTHTCPPCAPPELLGGPSVFLPPPKDITLMISR 266
Db 181 TCAASSGLMTKKNSTFVRVHEKPGDKTHTCPPCAPPELLGGPSVFLPPPKDITLMISR 240
Qy 267 TPEVTCVVVDVSHEDPEVKFNWYDGVVEVNAKTKPREEQNSTYRVVSVLTVLHQDLN 326
Db 241 TPEVTCVVVDVSHEDPEVKFNWYDGVVEVNAKTKPREEQNSTYRVVSVLTVLHQDLN 300
Qy 327 GKEYCKVSNKALPAPIETISKAKGQPRSPQVYTLPPSRDELTKNQVSLTCLVKGFYPS 386
Db 301 GKEYCKVSNKALPAPIETISKAKGQPRSPQVYTLPPSRDELTKNQVSLTCLVKGFYPS 360
Qy 387 DIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSKLTVDKSRWQGNVFSCSVHREALNHN 446
Db 361 DIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSKLTVDKSRWQGNVFSCSVHREALNHN 420
Qy 447 YTKQSLSLSPGK 458
Db 421 YTKQSLSLSPGK 432

RESULT 6
AAAY97595
ID AAAY97595 standard; protein; 455 AA.
XX
XX AC AAAY97595;
XX
XX 05-APR-2001 (first entry)
DT
DE
DE
XX Flt1 receptor fusion protein Flt1D2.VEGFR3D3.FcDeltaC1(a).
KW Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic;
KW plasma leakage; vascular permeability; IGF Fc region.
XX
XX Unidentified.
XX
XX WO200075319-A1.
XX

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PD 14-DEC-2000.  
XX  
XX  
PF 23-MAY-2000; 2000WO-US014142.  
XX  
XX  
PR 08-JUN-1999; 99US-0138133P.  
XX  
XX  
FA (REGE-) REGENERON PHARM INC.  
XX  
XX  
PI Papadopoulos NJ, Davis S, Yancopoulos GD;  
XX  
XX  
DR WPI; 2001-071076/08.  
DR  
DR N-PSDB; AAA91075.  
XX  
XX  
PT Nucleic acid molecule encoding mammalian phospholipid transfer protein,  
PT and its fragments, useful for diagnosis, evaluation, and treatment of  
PT diseases associated with the gene expression and for producing model  
PT systems.  
XX  
XX  
PS Claim 49; Fig 22; 159pp; English.  
XX  
XX  
CC This sequence represents a fusion protein of the invention between the  
CC Flt1 receptor and the Fc region of IgG. The specification relates to  
CC modified chimeric polypeptides with improved pharmacokinetics. The  
CC modified chimeric polypeptides are preferably Flt1 receptor polypeptides  
CC that have been modified to improve their pharmacokinetic profile. The  
CC polypeptides can be used to decrease or inhibit plasma leakage and/or  
CC vascular permeability in a mammal  
XX  
XX  
SQ Sequence 455 AA;  
  
Query Match 84.9%; Score 2069.5; DB 4; Length 455;  
Best Local Similarity 85.7%; Pred. No. 3e-129;  
Matches 395; Conservative 16; Mismatches 41; Indels 9; Gaps 3;  
  
Qy 1 MVSYWDGTGVLCCALLSCLLLTGSSGSDTGRPFVEMYSEIPIIHTMTEGRELVI PCRVTS 60  
Db. 1 MVSYWDGTGVLCCALLSCLLLTGSSG---GRPFVEMYSEIPIIHTMTEGRELVI PCRVTS 57  
  
Qy 61 PNITVTLKKPPLDTLIPDGKRIIWSRKGFIIISNATYKEIGLLTCEATVNGHLYKTNVLT 120  
Db 58 PNITVTLKKPPLDTLIPDGKRIIWSRKGFIIISNATYKEIGLLTCEATVNGHLYKTNVLT 117  
  
Qy 121 HROTNTIIDVLSFSGHIELSVGKLVNCTARTELNVGIDFNWEPSSKHQHKLVNRD 180  
Db 118 HROTNTIIDQLPRKSLLELVGKLVNCTVWAEFNSGVTDFWDYFGKQAEGRKWVPER 177  
  
Qy 181 LKQSGSEMKKFLSTLIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEK---DKTHTC 237  
Db 178 RSQQTHTFELS---SILTHNVSQHDLGSYVCANNNGIQRFRESTEVIHENGPGDKTHTC 234  
  
Qy 238 PPCAPALLGGPSVFLPFPKPDLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVVHN 297  
Db 235 PPCAPALLGGPSVFLPFPKPDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVVHN 294  
  
Qy 298 AKTPREEQYNSTYRVSVLTVLHQDLNGLKEYCKYVKSNKALPAPIETISKAKGQPREP 357  
Db 295 AKTPREEQYNSTYRVSVLTVLHQDLNGLKEYCKYVKSNKALPAPIETISKAKGQPREP 354  
  
Qy 358 QVYTLPSRDELTKQVSLCLVKGFYPSDIAVWESNGOPENNYKTTTPVLSDSGFFL 417  
Db 355 QVYTLPSRDELTKQVSLCLVKGFYPSDIAVWESNGOPENNYKTTTPVLSDSGFFL 414  
  
Qy 418 YSKLTVDKSRWQQGNVFCSCVMHEALNHHYTKSLSPGK 458  
Db 415 YSKLTVDKSRWQQGNVFCSCVMHEALNHHYTKSLSPGK 455  
  
RESULT 7  
ABP52448  
ID ABP52448 standard; protein; 455 AA.  
XX  
AC ABP52448;  
XX

DT 23-OCT-2002 (first entry)  
XX  
XX  
DE Modified Flt1 receptor Flt1D2.VEGFR3D3.FcDELTA1(a) protein sequence.  
XX  
XX  
KW Human; Flt1; vascular endothelial growth factor; VEGF; VEGF antagonist;  
KW psoriasis; wound healing; Flt1 receptor; antipsoriatic; antiinflammatory;  
KW vulnery; antiasthmatic; antirheumatic; antiarthritic; nephrotropic;  
KW ophthalmological; vascular permeability; oedema; inflammation; asthma;  
KW brain oedema; inflammatory disorder; rheumatoid arthritis; burn;  
KW kidney disease; eye disorder; age-related macular degeneration;  
KW diabetic retinopathy.  
XX  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
XX  
PN WO200260489-A1.  
XX  
XX  
PD 08-AUG-2002.  
XX  
XX  
PF 28-JAN-2002; 2002WO-US002466.  
XX  
XX  
PR 31-JAN-2001; 2001US-00773877.  
XX  
XX  
PA (REGE-) REGENERON PHARM INC.  
XX  
XX  
PI Xia Y, Rudge JS, Yancopoulos GD;  
XX  
XX  
DR WPI; 2002-608488/65.  
DR N-PSDB; ABQ74609.  
XX  
XX  
PT Treating psoriasis and enhancing wound healing in humans comprises the  
PT administration of a vascular endothelial cell growth factor (VEGF)  
PT antagonist.  
XX  
XX  
PS Example 17; Fig 22A-C; 179pp; English.  
XX  
XX  
CC The present invention describes a method for treating psoriasis and  
CC enhancing wound healing in a mammal or a human. The method comprises  
CC administering a vascular endothelial cell growth factor (VEGF) antagonist  
CC to the mammal or human. A VEGF antagonist has antipsoriatic,  
CC antiinflammatory, vulnery, antiasthmatic, antirheumatic, antiarthritic,  
CC nephrotropic and ophthalmological activities. The method can be used in  
CC treating psoriasis and enhancing wound healing in humans by administering  
CC VEGF antagonist. The method is also useful in treating clinical  
CC conditions characterised by vascular permeability, oedema or  
CC inflammation, such as brain oedema associated with injury, oedema  
CC associated with inflammatory disorders (e.g. rheumatoid arthritis),  
CC asthma, burns, kidney diseases, or eye disorders such as age-related  
CC macular degeneration and diabetic retinopathy. The method may also be  
CC used in making the polypeptide to decrease or inhibit plasma leakage and  
CC or vascular permeability. The present sequence represents  
CC Flt1D2.VEGFR3D3.FcDELTA1(a) which is used in an example from the present  
CC invention  
XX  
SQ Sequence 455 AA;  
  
Query Match 84.9%; Score 2069.5; DB 5; Length 455;  
Best Local Similarity 85.7%; Pred. No. 3e-129;  
Matches 395; Conservative 16; Mismatches 41; Indels 9; Gaps 3;  
  
Qy 1 MVSYWDGTGVLCCALLSCLLLTGSSGSDTGRPFVEMYSEIPIIHTMTEGRELVI PCRVTS 60  
Db. 1 MVSYWDGTGVLCCALLSCLLLTGSSG---GRPFVEMYSEIPIIHTMTEGRELVI PCRVTS 57  
  
Qy 61 PNITVTLKKPPLDTLIPDGKRIIWSRKGFIIISNATYKEIGLLTCEATVNGHLYKTNVLT 120  
Db 58 PNITVTLKKPPLDTLIPDGKRIIWSRKGFIIISNATYKEIGLLTCEATVNGHLYKTNVLT 117  
  
Qy 121 HROTNTIIDVLSFSGHIELSVGKLVNCTARTELNVGIDFNWEPSSKHQHKLVNRD 180  
Db 118 HROTNTIIDQLPRKSLLELVGKLVNCTVWAEFNSGVTDFWDYFGKQAEGRKWVPER 177  
  
Qy 181 LKQSGSEMKKFLSTLIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEK---DKTHTC 237  
XX

Db	178	RSQTHTELS-----SILTTIHNVSQHDLGYSVCKANNQIQRFESTEVIIVHENGPDKTHTC	234								
Qy	238	PPCPAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN	297								
Db	235	PPCPAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN	294								
Qy	298	AKTKPREEOYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP	357								
Db	295	AKTKPREEOYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP	354								
Qy	358	QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFL	417								
Db	355	QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFL	414								
Qy	418	YSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK	458								
Db	415	YSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK	455								
RESULT 8											
ID	AA97592	standard; protein; 462 AA.									
AC	AA97592;										
XX	05-APR-2001	(first entry)									
DT	Flt1 receptor fusion protein Mut3:Flt1(2-3)-Fc.										
DE											
KW	Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic;										
KW	plasma leakage; vascular permeability; IgG Fc region.										
XX	Unidentified.										
XX	WO200075319-A1.										
PN	14-DEC-2000.										
PD	23-MAY-2000;	2000WO-US014142.									
PF	08-JUN-1999;	99US-0138133P.									
PR	(REGE-) REGENERON PHARM INC.										
XX	Papadopoulos NJ, Davis S, Yancopoulos GD;										
PI	WPI; 2001-071076/08.										
DR	N-PSDB; AAA91072.										
XX	Nucleic acid molecule encoding mammalian phospholipid transfer protein,										
PT	and its fragments, useful for diagnosis, evaluation, and treatment of										
PT	diseases associated with the gene expression and for producing model										
PT	systems.										
XX	Claim 49; Fig 15; 159pp; English.										
PS	This sequence represents a fusion protein of the invention between the										
XX	Flt1 receptor and the Fc region of IgG. The specification relates to										
CC	modified chimeric polypeptides with improved pharmacokinetics. The										
CC	modified chimeric polypeptides are preferably Flt1 receptor polypeptides										
CC	that have been modified to improve their pharmacokinetic profile. The										
CC	polypeptides can be used to decrease or inhibit plasma leakage and/or										
CC	vascular permeability in a mammal										
XX	Sequence 462 AA;										
SQ	Query Match 84.1%; Score 2049; DB 4; Length 462; Best Local Similarity 84.2%; Pred. No. 7.1e-128; Matches 393; Conservative 13; Mismatches 47; Indels 14; Gaps 3;										
Qy	1	MVSYWDTGVLLCALLSCLLLTGSSSG--GRPFVEMYSEIPIIHTMTEGRELVIPCRVTS	60								

Db	1	MVSYWDTGVLLCALLSCLLLTGSSSG--GRPFVEMYSEIPIIHTMTEGRELVIPCRVTS	57				
Qy	61	PNITVTLKKFPDLTLIPDGKRIIWDSRKGFIIISNATYKEIGLLTCEATVNGHLTKTYLT	120				
Db	58	PNITVTLKKFPDLTLIPDGKRIIWDSRKGFIIISNATYKEIGLLTCEATVNGHLTKTYLT	117				
Qy	121	HRQTNIIIDVLSPSHSGHIELSGEKLVLNCTARTELNVLGIDFNWEYPSCKHQHKKLVNRD	180				
Db	118	HRQTNIIIDVQISTPRPVKLLRGHTLVLNCTATTPLNTRVQMTWSYFDEKNKRASVRRR-	176				
Qy	181	LKTSQSGSEMKKFLSLTITDGVTRSDOGLYTCAAASSGLMTKKNSTFVRVHEK-----	231				
Db	177	-IDQNSHANIFYSVLITIDKMNQNDKGLYTCRVSGSPFSKSVNTSVHLYDKAGGEPKSC	235				
Qy	232	DKTHTCCPCPAPELLGGPSVFLPPPKDKDTLMIISRTPEVTCVVVDVSHEDPEVKFNWYVD	291				
Db	236	DKTHTCCPCPAPELLGGPSVFLPPPKDKDTLMIISRTPEVTCVVVDVSHEDPEVKFNWYVD	295				
Qy	292	GVEVHNATKPREOYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK	353				
Db	296	GVEVHNATKPREOYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK	355				
Qy	352	GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLD	411				
Db	356	GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLD	415				
Qy	412	DGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK	458				
Db	416	DGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK	462				
RESULT 9							
ID	ABP52445	standard; protein; 462 AA.					
XX	ABP52445;						
XX	23-OCT-2002	(first entry)					
XX	Mutation 3 Flt1(2-3)-Fc protein sequence.						
DE							
KW	Human; Flt1; vascular endothelial growth factor; VEGF; VEGF antagonist;						
KW	psoriasis; wound healing; Flt1 receptor; antiproliferative; antiinflammatory;						
KW	vulnerary; antiasthmatic; antirheumatic; antiarthritic; nephrotropic;						
KW	ophthalmological; vascular permeability; oedema; inflammation; asthma;						
KW	brain oedema; inflammatory disorder; rheumatoid arthritis; burn;						
KW	kidney disease; eye disorder; age-related macular degeneration;						
XX	diabetic retinopathy.						
OS	Homo sapiens.						
OS	Synthetic.						
XX							
PN	WO200260489-A1.						
XX	08-AUG-2002.						
XX	28-JAN-2002;	2002WO-US002466.					
XX	31-JAN-2001;	2001US-00773877.					
XX	(REGE-) REGENERON PHARM INC.						
XX	Xia Y, Rudge JS, Yancopoulos GD;						
XX	WPI; 2002-608488/65.						
DR	N-PSDB; ABQ74606.						
XX	Treating psoriasis and enhancing wound healing in humans comprises the						
PT	administration of a vascular endothelial cell growth factor (VEGF)						
PT	antagonist.						
XX	Example 13; Fig 15A-C; 179pp; English.						
PS							
XX							

CC The present invention describes a method for treating psoriasis and  
 CC enhancing wound healing in a mammal or a human. The method comprises  
 CC administering a vascular endothelial cell growth factor (VEGF) antagonist  
 CC to the mammal or human. A VEGF antagonist has antipsoriatic,  
 CC anti-inflammatory, vulnary, antiasthmatic, antirheumatic, antiarthritic,  
 CC nephrotropic and ophthalmological activities. The method can be used in  
 CC treating psoriasis and enhancing wound healing in humans by administering  
 CC VEGF antagonist. The method is also useful in treating clinical  
 CC conditions characterised by vascular permeability, oedema or  
 CC inflammation, such as brain oedema associated with injury, oedema  
 CC associated with inflammatory disorders (e.g. rheumatoid arthritis),  
 CC asthma, burns, kidney diseases, or eye disorders such as age-related  
 CC macular degeneration and diabetic retinopathy. The method may also be  
 CC used in making the polypeptide to decrease or inhibit plasma leakage and  
 CC or vascular permeability. The present sequence represents Mut3:Flt1(2-3)  
 CC -Fc which is used in an example from the present invention  
 CC  
 CC  
 CC

SQ Sequence 462 AA;

Query Match 84.1%; Score 2049; DB 5; Length 462;  
 Best Local Similarity 84.2%; Pred. No. 7.1e-128;  
 Matches 393; Conservative 13; Mismatches 47; Indels 14; Gaps 3;  
 Qy 1 MVSWDGTGVLALLSCLLLTGSSGSDTGRPPFVEMYSEIPEIIMHTEGRELVI PCRVTS 60  
 Db 1 MVSWDGTGVLALLSCLLLTGSSGSDTGRPPFVEMYSEIPEIIMHTEGRELVI PCRVTS 57  
 Qy 61 PNITVTLKKPPLDTLIPDGKRIIWDNRKGFIIISNATYKEIGLLTCEATVNGHLYKTNVLT 120  
 Db 58 PNITVTLKKPPLDTLIPDGKRIIWDNRKGFIIISNATYKEIGLLTCEATVNGHLYKTNVLT 117  
 Qy 121 HRQTNTIIDVVLSPSHGIELSVGKLVNCTARTELNVGIDFNWEYPSKHQHKLVNRD 180  
 Db 118 HRQTNTIIDVQISTPRPVKLLRGHTLVNCTATTPLNTRVQMTWSYPDEKNKRASVRRR- 176  
 Qy 181 LKQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEK----- 231  
 Db 177 -IDQSNSHANIFYSVLTIDKQNKDGLYTCRVSRGSPFSKSVNTSVHIYDKAGPEPKSC 235  
 Qy 232 DKHTCTPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 291  
 Db 236 DKHTCTPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 295  
 Qy 292 GVEVHNAKTPREBQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 351  
 Db 296 GVEVHNAKTPREBQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 355  
 Qy 352 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 411  
 Db 356 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 415  
 Qy 412 DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKSLSPGK 458  
 Db 416 DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKSLSPGK 462

RESULT 10

AA97591  
 ID AA97591 standard; protein; 452 AA.

XX AC  
 AA97591;

XX DT  
 05-APR-2001 (first entry)

XX DE  
 Flt1 receptor fusion protein Mut2:Flt1(2-3deltaB)-Fc.

XX KW  
 Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic;  
 XX plasma leakage; vascular permeability; IgG Fc region.

XX OS  
 Unidentified.

XX PN  
 W0200075319-A1.

XX

PD 14-DEC-2000.  
 XX 23-MAY-2000; 2000WO-US014142.  
 XX 08-JUN-1999; 99US-0138133P.  
 XX (REGG-) REGENERON PHARM INC.  
 XX Papadopoulos NJ, Davis S, Yancopoulos GD;  
 XX WPI; 2001-071076/08.  
 DR N-PSDB; AAA91071.

XX Nucleic acid molecule encoding mammalian phospholipid transfer protein,  
 PT and its fragments, useful for diagnosis, evaluation, and treatment of  
 PT diseases associated with the gene expression and for producing model  
 PT systems.

XX Claim 49; Fig 14; 159pp; English.

XX This sequence represents a fusion protein of the invention between the  
 CC Flt1 receptor and the Fc region of IgG. The specification relates to  
 CC modified chimeric polypeptides with improved pharmacokinetics. The  
 CC modified chimeric polypeptides are preferably Flt1 receptor polypeptides  
 CC that have been modified to improve their pharmacokinetic profile. The  
 CC polypeptides can be used to decrease or inhibit plasma leakage and/or  
 CC vascular permeability in a mammal

XX SQ Sequence 452 AA;

Query Match 83.6%; Score 2038; DB 4; Length 452;  
 Best Local Similarity 83.9%; Pred. No. 3.7e-127;  
 Matches 392; Conservative 10; Mismatches 41; Indels 24; Gaps 3;

Qy 1 MVSWDGTGVLALLSCLLLTGSSGSDTGRPPFVEMYSEIPEIIMHTEGRELVI PCRVTS 60  
 Db 1 MVSWDGTGVLALLSCLLLTGSSGSDTGRPPFVEMYSEIPEIIMHTEGRELVI PCRVTS 57  
 Qy 61 PNITVTLKKPPLDTLIPDGKRIIWDNRKGFIIISNATYKEIGLLTCEATVNGHLYKTNVLT 120  
 Db 58 PNITVTLKKPPLDTLIPDGKRIIWDNRKGFIIISNATYKEIGLLTCEATVNGHLYKTNVLT 117  
 Qy 121 HRQTNTIIDVVLSPSHGIELSVGKLVNCTARTELNVGIDFNWEYPSKHQHKLVNRD 180  
 Db 118 HRQTNTIIDVQISTPRPVKLLRGHTLVNCTATTPLNTRVQMTWSYP-----D 165  
 Qy 181 LKQSGSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEK----- 231  
 Db 166 EIDQSNSHANIFYSVLTIDKQNKDGLYTCRVSRGSPFSKSVNTSVHIYDKAGPEPKSC 225  
 Qy 232 DKHTCTPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 291  
 Db 226 DKHTCTPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 285  
 Qy 292 GVEVHNAKTPREBQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 351  
 Db 286 GVEVHNAKTPREBQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 345  
 Qy 352 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 411  
 Db 346 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 405  
 Qy 412 DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKSLSPGK 458  
 Db 406 DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKSLSPGK 452

RESULT 11

ABP52444  
 ID ABP52444 standard; protein; 452 AA.

XX AC  
 ABP52444;

```

DT 23-OCT-2002 (first entry)
XX Mutation 2 Flt1(2-3 delta B)-Fc protein sequence.
DE Human; Flt1; vascular endothelial growth factor; VEGF; VEGF antagonist;
XX psoriasis; wound healing; Flt1 receptor; antipsoriatic; antiinflammatory;
XX vulnery; antiasthmatic; antirheumatic; antiarthritic; nephrotropic;
XX ophthalmological; vascular permeability; oedema; inflammation; asthma;
XX brain oedema; inflammatory disorder; rheumatoid arthritis; burn;
XX kidney disease; eye disorder; age-related macular degeneration;
XX diabetic retinopathy.
OS Homo sapiens.
OS Synthetic.
XX WO200260489-A1.
XX 08-AUG-2002.
XX 28-JAN-2002; 2002WO-US002466.
XX 31-JAN-2001; 2001US-0073877.
XX (REG-) REGENERON PHARM INC.
XX Xia Y, Rudge JS, Yancopoulos GD;
XX WPI; 2002-608488/65.
XX N-PSDB; ABQ74605.
XX Treating psoriasis and enhancing wound healing in humans comprises the
XX administration of a vascular endothelial cell growth factor (VEGF)
XX antagonist.
XX Example 12; Fig 14A-C; 179pp; English.
XX The present invention describes a method for treating psoriasis and
XX enhancing wound healing in a mammal or a human. The method comprises
XX administering a vascular endothelial cell growth factor (VEGF) antagonist
XX to the mammal or human. A VEGF antagonist has antipsoriatic,
XX antiinflammatory, vulnery, antiasthmatic, antirheumatic, antiarthritic,
XX nephrotropic and ophthalmological activities. The method can be used in
XX treating psoriasis and enhancing wound healing in humans by administering
XX VEGF antagonist. The method is also useful in treating clinical
XX conditions characterised by vascular permeability, oedema or
XX inflammation, such as brain oedema associated with injury, oedema
XX associated with inflammatory disorders (e.g. rheumatoid arthritis),
XX asthma, burns, kidney diseases, or eye disorders such as age-related
XX macular degeneration and diabetic retinopathy. The method may also be
XX used in making the polypeptide to decrease or inhibit plasma leakage and
XX or vascular permeability. The present sequence represents Mut2:Flt1(2-3
XX delta B)-Fc which is used in an example from the present invention
XX
XX Sequence 452 AA;
Query Match 83.6%; Score 2038; DB 5; Length 452;
Best Local Similarity 83.9%; Pred. No. 3.7e-127;
Matches 392; Conservative 10; Mismatches 41; Indels 24; Gaps 3;
QY 1 MVS YWDTGVLLCALLSGLLTGSSGSDTGRPFVMEYSEIPEIIMTEGRELVI PCRVTS 60
DB 1 MVS YWDTGVLLCALLSGLLTGSSG---GRPFVMEYSEIPEIIMTEGRELVI PCRVTS 57
QY 61 PNITVTLKKFPDLTLPDGKRII WDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNLT 120
DB 58 PNITVTLKKFPDLTLPDGKRII WDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNLT 117
QY 121 HRQNTIIDVVLSPSHGIEUSVGBKVLNCTARTELNVGIDFNWEYPSKQHKHKLWNRD 180
DB 118 HRQNTIIDVQISPRPVKLLRGHTLVNLTCTATTPLNTRVQMTWSPY-----D 165
QY 181 LKTOGSGEMKKFLSTLTIDGVTRSDQGLYGTCAASGSLMTKKNSTFVRVHEK----- 231

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Db 166 EIDQNSHANIFYSVLTIDKMQNKGLYTCRVSRSGSPKSVNTSVHIYDKAGPEPKSC 225
QY 232 DKTHTCPPCPAPPELLGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYD 291
Db 226 DKTHTCPPCPAPPELLGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYD 285
QY 292 GVEVHNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 351
Db 286 GVEVHNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 345
QY 352 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 411
Db 346 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 405
QY 412 DGSFFLYSKLTVDKSRWQQGNVPSVCSVMHEALHNHYTQKSLSLSPGK 458
Db 406 DGSFFLYSKLTVDKSRWQQGNVPSVCSVMHEALHNHYTQKSLSLSPGK 452
RESULT 12
AAV97593
ID AAV97593 standard; protein; 567 AA.
XX
AC AAV97593;
XX
DT 05-APR-2001 (first entry)
XX
DE Flt1 receptor fusion protein Mut4:Flt1(1-3R-N)-Fc.
XX
KW Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic;
KW plasma leakage; vascular permeability; IgG Fc region.
XX
OS Unidentified.
XX
PN WO200075319-A1.
XX
PD 14-DEC-2000.
XX
PF 23-MAY-2000; 2000WO-US014142.
XX
PR 08-JUN-1999; 99US-0138133P.
XX
PA (REG-) REGENERON PHARM INC.
XX
PI Papadopoulos NJ, Davis S, Yancopoulos GD;
XX
XX WPI; 2001-071076/08.
XX N-PSDB; AAA91073.
XX
XX Nucleic acid molecule encoding mammalian phospholipid transfer protein,
XX and its fragments, useful for diagnosis, evaluation, and treatment of
XX diseases associated with the gene expression and for producing model
XX systems.
XX
XX Claim 49; Fig 16; 159pp; English.
XX
XX This sequence represents a fusion protein of the invention between the
XX Flt1 receptor and the Fc region of IgG. The specification relates to
XX modified chimeric polypeptides with improved pharmacokinetics. The
XX modified chimeric polypeptides are preferably Flt1 receptor polypeptides
XX that have been modified to improve their pharmacokinetic profile. The
XX polypeptides can be used to decrease or inhibit plasma leakage and/or
XX vascular permeability in a mammal
XX
XX Sequence 567 AA;
Query Match 82.7%; Score 2015.5; DB 4; Length 567;
Best Local Similarity 89.6%; Pred. No. 1.5e-125;
Matches 396; Conservative 14; Mismatches 46; Indels 113; Gaps 3;
QY 1 MVS YWDTGVLLCALLSGLLTGSSG----- 26
DB 1 MVS YWDTGVLLCALLSGLLTGSSGSKLKDPELSLKGTHQIMQAGOTLHLCRGEAAHK 60

```



QY 27 ----- 26  
 Db 61 WSLPEMVSKESERLSITKSGRNGKQFCSTLTNTAQANHTGFYSCKYLAVPTSKKET 120  
 QY 27 -----SDTGRPFVEMYSEIPEIIHMTGRELIVICRVTSPTNITVTLKKFPLDTLPD 78  
 Db 121 ESAIYIFISDTGRPFVEMYSEIPEIIHMTGRELIVICRVTSPTNITVTLKKFPLDTLPD 180  
 QY 79 GKRIIWSRKGFIISNATYKEIGLLTCEATVNGHLYKTNLYTHRQNTIIDVLSPSHGI 138  
 Db 181 GKRIIWSRKGFIISNATYKEIGLLTCEATVNGHLYKTNLYTHRQNTIIDVQISTPRPV 240  
 QY 139 ELSVGEKLVNCTARTLNVDGFNWEYPSKQHKHKLNVNRDLTKTQSGSEMKKFLSTLTI 198  
 Db 241 KLLRGHTLVNCTATTPLNTRVQMTWSYPDEKKNASVRRR--IDQSNSHANIFYSVLTI 298  
 QY 199 DGVTRSDQGLYTCAASGLMTKKNSTFVRVHEK-----DKHTCTPCCPAPPELLGGP 249  
 Db 299 DKMQNDKGLYTCRVRSGPSFKSVNTSVHIYDKAGPGEKSCDKTHTCCPCPAPPELLGGP 358  
 QY 250 SVFLFPPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEOYNS 309  
 Db 359 SVFLFPPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEOYNS 418  
 QY 310 TYRVSVSLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSDEL 369  
 Db 419 TYRVSVSLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSDEL 478  
 QY 370 TKQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSRWQ 429  
 Db 479 TKQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSRWQ 538  
 QY 430 QGNVFSCVMHEALHNHYTQKSLSLSPGK 458  
 Db 539 QGNVFSCVMHEALHNHYTQKSLSLSPGK 567

## RESULT 13

ABP52446  
 ID ABP52446 standard; protein; 567 AA.

XX ABP52446;

XX AC  
 XX DT 23-OCT-2002 (first entry)

XX DE Mutation 4 Flt1(2-3 R-N)-Fc protein sequence.

XX KW Human; Flt1; vascular endothelial growth factor; VEGF; VEGF antagonist;  
 KW psoriasis; wound healing; Flt1 receptor; antipsoriatic; antiinflammatory;  
 KW vulnary; antiasthmatic; antirheumatic; antiarthritic; nephrotropic;  
 KW ophthalmological; vascular permeability; oedema; inflammation; asthma;  
 KW brain oedema; inflammatory disorder; rheumatoid arthritis; burn;  
 KW kidney disease; eye disorder; age-related macular degeneration;  
 KW diabetic retinopathy.

XX OS Homo sapiens.  
 OS Synthetic.

XX PN WO200260489-A1.

XX PD 08-AUG-2002.

XX PF 28-JAN-2002; 2002WO-US002466.

XX PR 31-JAN-2001; 2001US-00773877.

XX PA (REG-1) REGENERON PHARM INC.

XX PI Xia Y, Rudge JS, Yancopoulos GD;

XX DR WPI; 2002-608488/65.

XX DR N-PSDB; ABQ74607.

XX Treating psoriasis and enhancing wound healing in humans comprises the  
 PT administration of a vascular endothelial cell growth factor (VEGF)  
 PT antagonist.

XX Example 14; Fig 16A-D; 179pp; English.

XX The present invention describes a method for treating psoriasis and  
 CC enhancing wound healing in a mammal or a human. The method comprises  
 CC administering a vascular endothelial cell growth factor (VEGF) antagonist  
 CC to the mammal or human. A VEGF antagonist has antipsoriatic,  
 CC antiinflammatory, vulnerary, antiasthmatic, antirheumatic, antiarthritic,  
 CC nephrotropic and ophthalmological activities. The method can be used in  
 CC treating psoriasis and enhancing wound healing in humans by administering  
 CC VEGF antagonist. The method is also useful in treating clinical  
 CC conditions characterised by vascular permeability, oedema or  
 CC inflammation, such as brain oedema associated with injury, oedema  
 CC associated with inflammatory disorders (e.g. rheumatoid arthritis),  
 CC asthma, burns, kidney diseases, or eye disorders such as age-related  
 CC macular degeneration and diabetic retinopathy. The method may also be  
 CC used in making the polypeptide to decrease or inhibit plasma leakage and  
 CC or vascular permeability. The present sequence represents Mut4:Flt1(2-3 R  
 CC -N)-Fc which is used in an example from the present invention  
 XX SQ Sequence 567 AA;

Query Match 82.7%; Score 2015.5; DB 5; Length 567;

Best Local Similarity 69.6%; Pred. No. 1.5e-125; Indels 113; Gaps 3;

Matches 396; Conservative 14; Mismatches 46;

QY 1 MVSVDYDGVLLCALLSCLLLTGSSSG----- 26

Db 1 MVSVDYDGVLLCALLSCLLLTGSSSGKLDPELSLKGTHQIMQAGOTLHLQCRGEAAHK 60

QY 27 ----- 26

Db 61 WSLPEMVSKESERLSITKSGRNGKQFCSTLTNTAQANHTGFYSCKYLAVPTSKKET 120

QY 27 -----SDTGRPFVEMYSEIPEIIHMTGRELIVICRVTSPTNITVTLKKFPLDTLPD 78

Db 121 ESAIYIFISDTGRPFVEMYSEIPEIIHMTGRELIVICRVTSPTNITVTLKKFPLDTLPD 180

QY 79 GKRIIWSRKGFIISNATYKEIGLLTCEATVNGHLYKTNLYTHRQNTIIDVLSPSHGI 138

Db 181 GKRIIWSRKGFIISNATYKEIGLLTCEATVNGHLYKTNLYTHRQNTIIDVQISTPRPV 240

QY 139 ELSVGEKLVNCTARTLNVDGFNWEYPSKQHKHKLNVNRDLTKTQSGSEMKKFLSTLTI 198

Db 241 KLLRGHTLVNCTATTPLNTRVQMTWSYPDEKKNASVRRR--IDQSNSHANIFYSVLTI 298

QY 199 DGVTRSDQGLYTCAASGLMTKKNSTFVRVHEK-----DKHTCTPCCPAPPELLGGP 249

Db 299 DKMQNDKGLYTCRVRSGPSFKSVNTSVHIYDKAGPGEKSCDKTHTCCPCPAPPELLGGP 358

QY 250 SVFLFPPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEOYNS 309

Db 359 SVFLFPPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEOYNS 418

QY 310 TYRVSVSLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSDEL 369

Db 419 TYRVSVSLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSDEL 478

QY 370 TKQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSRWQ 429

Db 479 TKQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSRWQ 538

QY 430 QGNVFSCVMHEALHNHYTQKSLSLSPGK 458

Db 539 QGNVFSCVMHEALHNHYTQKSLSLSPGK 567

RESULT 14

AA97597

ID	AAAY97597 standard; protein; 567 AA.	QY	250	SVFLFPKPKD	TLIMISRTPEVT	CVVVDVSHEDPEVKFNWYDGV	VHNAKTKPREQYNS	309
AC	AAAY97597;	Db	359	SVFLFPKPKD	TLIMISRTPEVT	CVVVDVSHEDPEVKFNWYDGV	VHNAKTKPREQYNS	418
XX	05-APR-2001 (first entry)	QY	310	TYRVSVLTVL	HQDWLNGKEY	CKVSNKALPAPIEKT	ISKAKGQPREPQVYTLPPSRDEL	369
XX	Flt1 receptor fusion protein Flt1(1-3)-Fc.	Db	419	TYRVSVLTVL	HQDWLNGKEY	CKVSNKALPAPIEKT	ISKAKGQPREPQVYTLPPSRDEL	478
XX	Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic;	QY	370	TKNQVSLTCL	VKGFPYSDIA	VEWESNGQPENNYKTTTPPV	LDSDGSFSLYSLKLTVDKSRWQ	429
KW	plasma leakage; vascular permeability; I9G Fc region.	Db	479	TKNQVSLTCL	VKGFPYSDIA	VEWESNGQPENNYKTTTPPV	LDSDGSFSLYSLKLTVDKSRWQ	538
XX	Unidentified.	QY	430	QGNVFSCSV	MHEALHNHYT	QKSLSLSPGK	458	
XX	WO200075319-A1.	Db	539	QGNVFSCSV	MHEALHNHYT	QKSLSLSPGK	567	
XX	14-DEC-2000.							
XX	23-MAY-2000; 2000WO-US014142.							
XX	08-JUN-1999; 99US-0138133P.							
XX	(REGE-) REGENERON PHARM INC.							
PI	Papadopoulos NJ, Davis S, Yancopoulos GD;							
XX	WPI; 2001-071076/08.							
DR	N-PSDB; AAA91077.							
XX	Nucleic acid molecule encoding mammalian phospholipid transfer protein,							
PT	and its fragments, useful for diagnosis, evaluation, and treatment of							
PT	diseases associated with the gene expression and for producing model							
PT	systems.							
XX	Example 11; Fig 10; 159pp; English.							
PS	This sequence represents a fusion protein of the invention between the							
CC	Flt1 receptor and the Fc region of IgG. The specification relates to							
CC	modified chimeric polypeptides with improved pharmacokinetics. The							
CC	modified chimeric polypeptides are preferably Flt1 receptor polypeptides							
CC	that have been modified to improve their pharmacokinetic profile. The							
CC	polypeptides can be used to decrease or inhibit plasma leakage and/or							
CC	vascular permeability in a mammal							
XX	Sequence 567 AA;							
SQ	Query Match 82.7%; Score 2014.5; DB 4; Length 567;							
	Best Local Similarity 69.6%; Pred. No. 1.8e-125;							
	Matches 396; Conservative 13; Mismatches 47; Indels 113; Gaps 3;							
QY	1 MVS YWDTGVLLCALLSCLLLTGSSG-----	26						
Db	1 MVS YWDTGVLLCALLSCLLLTGSSGSKLDPKLSLKGTHQIMQAGQTLHLQCRGEAAHK	60						
QY	27 -----	26						
Db	61 WSLPEMVSKESERLSITKACGRNGKQFCSTLTLNTAQANHTGFYSCKYLAVTSKKET	120						
QY	27 -----SDTGRPFVEMYSEIPEIIHMTGRELIVPCRVTSPTNITVTLKKFPLDTLPD	78						
Db	121 ESAIYIIFISDTGRPFVEMYSEIPEIIHMTGRELIVPCRVTSPTNITVTLKKFPLDTLPD	180						
QY	79 GKRIIWSRGFIISNATYKEIGLLTCEATVNGHLYKTNLTTHRTQNTIIDVVLSPSHGI	138						
Db	181 GKRIIWSRGFIISNATYKEIGLLTCEATVNGHLYKTNLTTHRTQNTIIDVQISTPRPV	240						
QY	139 ELSVGEKVLNCTARTLNVDNWEYPPSSKHQKHLVNRDLKTQSGSEMKKFLSLTI	198						
Db	241 KLURGHTVLNCTATTLNTRVQMTWSYDEKNKRASVRRR--IDQNSNANIFYSVLTI	298						
QY	199 DGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEK-----DKHTPCPCPAPELLGGP	249						
Db	299 DKMQNDKGLYTCRVSRGSPFSKSVNTSVHIYDKAGPGPKSCDKTHTCPCPAPELLGGP	358						

QY	250	SVFLFPKPKD	TLIMISRTPEVT	CVVVDVSHEDPEVKFNWYDGV	VHNAKTKPREQYNS	309
Db	359	SVFLFPKPKD	TLIMISRTPEVT	CVVVDVSHEDPEVKFNWYDGV	VHNAKTKPREQYNS	418
QY	310	TYRVSVLTVL	HQDWLNGKEY	CKVSNKALPAPIEKT	ISKAKGQPREPQVYTLPPSRDEL	369
Db	419	TYRVSVLTVL	HQDWLNGKEY	CKVSNKALPAPIEKT	ISKAKGQPREPQVYTLPPSRDEL	478
QY	370	TKNQVSLTCL	VKGFPYSDIA	VEWESNGQPENNYKTTTPPV	LDSDGSFSLYSLKLTVDKSRWQ	429
Db	479	TKNQVSLTCL	VKGFPYSDIA	VEWESNGQPENNYKTTTPPV	LDSDGSFSLYSLKLTVDKSRWQ	538
QY	430	QGNVFSCSV	MHEALHNHYT	QKSLSLSPGK	458	
Db	539	QGNVFSCSV	MHEALHNHYT	QKSLSLSPGK	567	
RESULT 15						
ABP52442						
ID	ABP52442 standard; protein; 567 AA.					
XX	AC	ABP52442;				
XX	DT	23-OCT-2002 (first entry)				
XX	DE	Flt1(1-3)-Fc protein sequence.				
XX	KW	Human; Flt1; vascular endothelial growth factor; VEGF; VEGF antagonist;				
KW	psoriasis; wound healing; Flt1 receptor; antipsoriatic; antiinflammatory;					
KW	vulnerary; antiasthmatic; antirheumatic; antiarthritic; nephrotropic;					
KW	ophthalmological; vascular permeability; oedema; inflammation; asthma;					
KW	brain oedema; inflammatory disorder; rheumatoid arthritis; burn;					
KW	kidney disease; eye disorder; age-related macular degeneration;					
KW	diabetic retinopathy.					
XX	Homo sapiens.					
OS	Synthetic.					
XX	FN	WO200260489-A1.				
XX	PD	08-AUG-2002.				
XX	PF	28-JAN-2002; 2002WO-US002466.				
XX	PR	31-JAN-2001; 2001US-00773877.				
XX	PA	(REGE-) REGENERON PHARM INC.				
PI	Xia Y, Rudge JS, Yancopoulos GD;					
XX	WPI; 2002-608488/65.					
DR	N-PSDB; ABQ74603.					
XX	Treating psoriasis and enhancing wound healing in humans comprises the					
PT	administration of a vascular endothelial cell growth factor (VEGF)					
PT	antagonist.					
XX	Example 11; Fig 10A-D; 179pp; English.					
PS	The present invention describes a method for treating psoriasis and					
XX	enhancing wound healing in a mammal or a human. The method comprises					
CC	administering a vascular endothelial cell growth factor (VEGF) antagonist					
CC	to the mammal or human. A VEGF antagonist has anticyporiatic,					
CC	antiinflammatory, vulnary, antisthmatic, antirheumatic, antiarthritic,					
CC	nephrotropic and ophthalmological activities. The method can be used in					
CC	treating psoriasis and enhancing wound healing in humans by administering					
CC	VEGF antagonist. The method is also useful in treating clinical					
CC	conditions characterised by vascular permeability, oedema or					
CC	inflammation, such as brain oedema associated with injury, oedema					
CC	associated with inflammatory disorders (e.g. rheumatoid arthritis),					
CC	asthma, burns, kidney diseases, or eye disorders such as age-related					
CC	macular degeneration and diabetic retinopathy. The method may also be					
CC	used in making the polypeptide to decrease or inhibit plasma leakage and					

CC or vascular permeability. The present sequence represents Flt1(1-3)-Fc  
CC which is used in an example from the present invention

XX  
SQ Sequence 567 AA;

```
Query Match      82.7%; Score 2014.5; DB 5; Length 567;
Best Local Similarity 69.6%; Pred.No.1.8e-125;
Matches 396; Conservative 13; Mismatches 47; Indels 113; Gaps 3;

Qy 1 MVS YWDTGVLLCALLCLLLTGSSSG----- 26
Db 1 MVS YWDTGVLLCALLCLLLTGSSSGSKLDPELSLKGTOHIMQAGQTLHLQCRGEAAHK 60
Qy 27 ----- 26
Db 27 ----- 26
Db 61 WSLPEMVSKESERLSITKACGRNGKQFCSTLTNTAQANHTGFYSCKYLAVPTSKKET 120
Qy 27 -----SDTGRPFVEMYSEIPEIIHMTGRELVIICRVTSFNITVTLKKFPLDTLIPD 78
Db 121 ESAIYIFISDTGRPFVEMYSEIPEIIHMTGRELVIICRVTSFNITVTLKKFPLDTLIPD 180
Qy 79 GKRIIWSRKGFIISNATYKEIGLLTCEATVNGHLYKTNVLTHTQNTIIDVVLSPSHGI 138
Db 181 GKRIIWSRKGFIISNATYKEIGLLTCEATVNGHLYKTNVLTHTQNTIIDVQISTPRPV 240
Qy 139 ELSVGEKLVNCTARTLNAGIDFNWEYPSKQHKKLVNRDLKTQSGSEMKKFLSTLTI 198
Db 241 KLLRGHTLVNCTATTPLNTRVQMTWSYPDEKNKRASVRRR--IDQSNSHANIFYSVLTI 298
Qy 199 DGVTRSDOGLYTCNASSGLMTKKNSTFVRVHEK-----DKTHTCPCPAPELLGGP 249
Db 299 DKMQNDKDGUYTCRVSRGSPFKSVNTSVHIYDKAGPGEPKSCDKTHTCPCPAPELLGGP 358
Qy 250 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 309
Db 359 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 418
Qy 310 TYRVVSVLTVQLHQLDNLGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDEL 369
Db 419 TYRVVSVLTVQLHQLDNLGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDEL 478
Qy 370 TKQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRWQ 429
Db 479 TKQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRWQ 538
Qy 430 QGNVFCSCVMHEALHNHYTOKSLSLSPGK 458
Db 539 QGNVFCSCVMHEALHNHYTOKSLSLSPGK 567
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Search completed: September 23, 2005, 17:14:53  
Job time : 125 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 23, 2005, 16:52:28 ; Search time 39 Seconds  
(without alignments)

1129.930 Million cell updates/sec

Title: US-10-811-170-2

Perfect score: 2437

Sequence: 1 MVSYDPTGVLLCALLSCLLL.....MHEALHHYTKSLSPGK 458

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1240.5	50.9	330	1 GHU	Ig gamma-1 chain C
2	1240.5	50.9	374	2 S69339	Ig heavy chain V r
3	1233	50.6	255	4 S31866	Ig gamma-1 chain C
4	1180	48.4	234	2 PT0207	Ig gamma chain C r
5	1148.5	47.1	326	1 G2HU	Ig gamma-2 chain C
6	1146	47.0	377	2 A23511	Ig gamma-3 chain C
7	1144	46.9	327	1 G4HU	Ig gamma-4 chain C
8	1144	46.9	377	2 A60764	Ig gamma-3 chain C
9	1121	46.0	289	1 G3HUI	Ig gamma-3 heavy c
10	929.5	38.1	328	2 I47160	Ig gamma 2b chain
11	929.5	38.1	328	2 I47159	Ig gamma 2a chain
12	925.5	38.0	323	1 GHRB	Ig gamma chain C r
13	917.5	37.6	277	2 I47162	Ig gamma 4 chain c
14	913.5	37.5	328	2 I47158	Ig gamma 1 chain c
15	900	36.9	329	1 G2GP	Ig gamma-2 chain C
16	899.5	36.9	328	2 I47161	Ig gamma 3 chain c
17	870	35.7	470	2 S22080	Ig heavy chain pre
18	866.5	35.6	329	1 G3MSC	Ig gamma-3 chain C
19	863.5	35.4	472	2 S31459	Ig gamma-1 chain -
20	855.5	35.1	398	1 G3MSM	Ig gamma-3 chain C
21	854.5	35.1	444	2 FC4436	monoclonal antibod
22	852	35.0	308	2 C30554	Ig heavy chain C r
23	844	34.6	333	2 PS0018	Ig gamma-2b chain
24	843.5	34.6	469	2 S37483	Ig gamma-2a chain
25	837.5	34.4	330	1 G2MSA	Ig gamma-1 chain C
26	833.5	34.2	324	1 G1MS	Ig gamma-1 chain C
27	832.5	34.2	399	1 G2MSGAM	Ig gamma-2c chain
28	832	34.1	329	2 S00847	Ig gamma-2c chain
29	831.5	34.1	326	2 PS0017	Ig gamma-1 chain C

RESULT 1

GHU

Ig gamma-1 chain C region - human

C;Species: Homo sapiens (man)

C;Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 09-Jul-2004

C;Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146

R;Ellison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A;Title: The nucleotide sequence of a human immunoglobulin C-gamma gene.

A;Reference number: A93433; MUID:82274238; PMID:6287432

A;Accession: A93433

A;Molecule type: DNA

A;Residues: 1-330 <ELL>

A;Cross-references: UNIPROT:P01857; EMBL:Z17370

A;Note: this sequence has the Gln(17) allotypic marker, 97-Lys, and the Gln(1) markers,

R;Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of a

A;Reference number: S33887; MUID:83001943; PMID:6811139

A;Accession: S33887

A;Molecule type: DNA

A;Residues: 88-113;235-330 <TAK>

A;Cross-references: EMBL:Z17370

R;Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, G.M.

Biochemistry 9, 3161-3170, 1970

A;Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen

A;Reference number: A90563; MUID:71064024; PMID:5489771

A;Contents: myeloma protein Eu

A;Accession: B90563

A;Molecule type: protein

A;Residues: 1-96,'R',98-135 <GUN>

A;Note: this sequence has the Gln(3) marker, 97-Arg

R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.

Biochemistry 9, 3171-3181, 1970

A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequen

A;Reference number: A90564; MUID:71064025; PMID:5530842

A;Contents: Eu

A;Accession: A90564

A;Molecule type: protein

A;Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',240,

A;Note: this sequence has the Gln(non-1) markers, 239-Glu and 241-Net

R;Fonstingl, H.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976

A;Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),

Ig gamma-1 chain C  
Ig gamma-2a chain  
Ig gamma-2a chain  
Ig gamma-2b chain  
Ig gamma-2a chain  
Ig gamma-2b chain  
soluble vascular e  
protein-tyrosine k  
Ig gamma-2b chain C  
Ig gamma-2 chain C  
protein-tyrosine k  
Ig gamma heavy cha  
Fit-1 tyrosine kin  
receptor tyrosine  
embryonic receptor  
Ig heavy chain V-I

ALIGNMENTS

igen Primaerstruktur.  
A:Reference number: A91668; MUID:77070269; PMID:826475  
A:Contents: myeloma protein Nie  
A:Accession: B91668  
A:Molecule type: protein  
A:Residues: 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QY 292 GVEVHNAKTPREQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 351  
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QY 352 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 411  
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## RESULT 4

PT0207  
Ig gamma chain C region - chimpanzee  
C;Species: Pan troglodytes (chimpanzee)  
C;Date: 23-Nov-1991 #sequence\_revision 23-Nov-1991 #text\_change 16-Jul-1999  
C;Accession: PT0207  
R;Enrich, P.H.; Moustafa, Z.A.; Oestberg, L.  
Mol. Immunol. 28, 319-322, 1991  
A;Title: Nucleotide sequence of chimpanzee Fc and hinge regions.  
A;Reference number: PT0207; MUID:91287716; PMID:2062315  
A;Accession: PT0207  
A;Molecule type: mRNA  
A;Residues: 1-234 <EHR>  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;48-117/Domain: immunoglobulin homology <IM>

Query Match 48.4%; Score 1180; DB 2; Length 234;  
Best Local Similarity 98.6%; Pred. No. 6e-68;  
Matches 217; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 232 DKTHTCPPCAPLGGSPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 291  
Db 15 DTHTTCCPCAPLGGSPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 74  
QY 292 GVEVHNAKTPREQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 351  
Db 75 GVEVHNAKTPREQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 134  
QY 352 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 411  
Db 135 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 194  
QY 412 DGSFFLYSKLTVDKSRWQQGNVSCSMHEALHNYTKQSLSPGK 451  
Db 195 DGSFFLYSKLTVDKSRWQQGNVSCSMHEALHNYTKQSLSPGK 234

## RESULT 5

G2HU  
Ig gamma-2 chain C region - human  
C;Species: Homo sapiens (man)  
C;Date: 30-Apr-1981 #sequence\_revision 13-Jun-1983 #text\_change 09-Jul-2004  
C;Accession: A93906; A92809; A90752; A93132; A02148  
R;Ellison, J.; Hood, L.  
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982  
A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con  
A;Reference number: A93906; MUID:82197621; PMID:6804948  
A;Accession: A93906  
A;Molecule type: DNA  
A;Residues: 1-326 <ELL>  
A;Cross-references: UNIPROT:P01859; GB:V00554; GB:J00230; NID:G32759; PIDN:CAB58438.1; F  
A;Note: Lys-326 is probably removed posttranslationally  
R;Wang, A.C.; Tung, E.; Fudenberg, H.H.  
J. Immunol. 125, 1048-1054, 1980  
A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f

A;Reference number: A92809; MUID:81007873; PMID:6774012  
A;Contents: myeloma protein Til  
A;Accession: A92809  
A;Molecule type: protein  
A;Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>  
A;Note: Trp-156 is at or near the complement-binding site  
R;Connell, G.E.; Parr, D.M.; Hofmann, T.  
Can. J. Biochem. 57, 758-767, 1979  
A;Title: The amino acid sequences of the three heavy chain constant region domains of a t  
A;Reference number: A90752; MUID:80001357; PMID:113060  
A;Contents: myeloma protein Zie  
A;Accession: A90752  
A;Molecule type: protein  
A;Residues: 1-24, 'E', 26-57, 'EV', 60-85, 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-2  
R;Hofmann, T.; Parr, D.M.  
Mol. Immunol. 16, 923-925, 1979  
A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin ga  
A;Reference number: A93132; MUID:80114419; PMID:118920  
A;Contents: Zie  
A;Accession: A93132  
A;Molecule type: protein  
A;Residues: 238-275 <HOF>  
R;Hofmann, T.; Parr, D.M.  
submitted to the Atlas, March 1980  
A;Reference number: A94591  
A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268  
A;Note: the revised sequence differs from that shown in having 60-Ala and in the amidatio  
ned  
R;Milstein, C.; Frangione, B.  
Biochem. J. 121, 217-225, 1971  
A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.  
A;Reference number: A90253; MUID:72033500; PMID:4940472  
A;Contents: annotation; myeloma protein Sa, disulfide bonds  
R;Frangione, B.; Milstein, C.; Pink, J.R.L.  
Nature 221, 145-148, 1969  
A;Title: Structural studies of immunoglobulin G.  
A;Reference number: A93157; MUID:69064124; PMID:5782707  
A;Contents: annotation; Sa, disulfide bonds  
C;Genetics:  
A;Gene: GDB:IGHG2  
A;Cross-references: GDB:119338; OMIM:147110  
A;Map position: 14q32.33-14q32.33  
A;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F;133-202/Domain: immunoglobulin homology <IM1>  
F;20-85/Domain: immunoglobulin homology <IM2>  
F;239-306/Domain: immunoglobulin homology <IM3>  
F;14/Disulfide bonds: interchain (to light chain) #status experimental  
F;27-83, 140-200, 246-304/Disulfide bonds: #status experimental  
F;102, 103, 106, 109/Disulfide bonds: interchain (to heavy chain) #status experimental  
F;176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 47.1%; Score 1148.5; DB 1; Length 326;  
Best Local Similarity 80.0%; Pred. No. 9e-66;  
Matches 224; Conservative 13; Mismatches 20; Indels 23; Gaps 6;

QY 197 TIDGVTSDQGLYTCGAASGLMTKKNSTF-----VRVHEK-----DKT-----HTCP 238  
Db 52 TTPAVLQS--SGLYSL---SSVVTVPSSNFGTQTYTCNVDPKPSNTKVDKTVKCCVCEP 107  
QY 239 PCPAPPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNA 298  
Db 108 PCPAPP--VAGSPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNA 166  
QY 299 KTKPREQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 358  
Db 167 KTKPREQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 226  
QY 359 VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLY 418

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Db      227 VYTLPPSRREMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPMLDSDGSFFLY 286
QY      419 SKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 458
Db      287 SKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 326

RESULT 6
A23511
IG gamma-3 chain C region (allotype G3m(b)) - human
C:Species: Homo sapiens (man)
C>Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C:Accession: A23511
R:Huck, S.; Port, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: c
A:Reference number: A23511; MUID:86148507; PMID:3081877
A:Accession: A23511
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
A:Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
C:Genetics:
A:Gene: GDB:IGHG3
A:Cross-references: GDB:119339; OMIM:147120
A:Map position: 14q32.33-14q32.33
A:Introns: 98/3; 113/3; 130/3; 145/3; 160/3; 270/3
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM>

Query Match      47.0%; Score 1146; DB 2; Length 377;
Best Local Similarity 92.5%; Pred. No. 1.5e-65;
Matches 210; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY      232 DKTHTCPPCPAPBLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 291
Db      151 DTPPPCPRCFAPBLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 210

QY      292 GVEVHNAKTKPREQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK 351
Db      211 GVEVHNAKTKPREQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKTK 270

QY      352 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 411
Db      271 GQPREPQVYTLPPSRDEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTPPMLDS 330

QY      412 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 458
Db      331 DGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNRTQKSLSLSPGK 377

RESULT 7
G4HU
IG gamma-4 chain C region - human
C:Species: Homo sapiens (man)
C>Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004
C:Accession: A90933; A90249; A02150
R:Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A:Reference number: A90933; MUID:83157104; PMID:6299662
A:Accession: A90933
A:Molecule type: DNA
A:Residues: 1-327 <ELL>
A:Cross-references: UNIPROT:P01861
A>Note: the sequence was determined from the germline gene
R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A:Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant
A:Reference number: A90249; MUID:70207560; PMID:4192699
A:Accession: A90249
A:Molecule type: protein
A:Residues: 1-30;81-326 <PIN>

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C:Genetics:
A:Gene: GDB:IGHG4
A:Cross-references: GDB:119340; OMIM:147130
A:Map position: 14q32.33-14q32.33
A:Introns: 99/1; 111/1; 221/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:99-110/Region: hinge
F:134-203/Domain: immunoglobulin homology <IM2>
F:240-307/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: interchain (to light chain) #status experimental
F:27-83;141-201;247-305/Disulfide bonds: #status predicted
F:106;109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      46.9%; Score 1144; DB 1; Length 327;
Best Local Similarity 79.9%; Pred. No. 1.7e-65;
Matches 222; Conservative 14; Mismatches 24; Indels 18; Gaps 4;

QY      197 TIDGVTSRDQGLYTCAA-----SSGLMTKKNSTFVRVHEKDKTHT-----CPPC 240
Db      52 TFPVAVLQS-SGLYSLSSVTVVSSSLGTYTCYD-HKPSNTKVDKRVESKVGPPCPSC 109

QY      241 PAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 300
Db      110 PAPEFLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 169

QY      301 KPREQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKQPREPOVY 360
Db      170 KPREQNFSTYRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTISKAKQPREPOVY 229

QY      361 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 420
Db      230 TLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSR 289

QY      421 LTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 458
Db      290 LTVDKSRWQEGNVFCSCVMHEALHNHYTQKSLSLGLK 327

RESULT 8
A60764
IG gamma-3 chain C region, form LAT - human
C:Species: Homo sapiens (man)
C>Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004
C:Accession: A60764
R:Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A:Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 convert
A:Reference number: A60764; MUID:90007613; PMID:2571587
A:Accession: A60764
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
A:Cross-references: UNIPROT:Q8N4Y9
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:20-85/Domain: immunoglobulin homology <IMM>

Query Match      46.9%; Score 1144; DB 2; Length 377;
Best Local Similarity 92.5%; Pred. No. 2.1e-65;
Matches 210; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY      232 DKTHTCPPCPAPBLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 291
Db      151 DTPPPCPRCFAPBLGGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 210

QY      292 GVEVHNAKTKPREQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK 351
Db      211 GVEVHNAKTKPREQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKTK 270

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Db      64  DTTPPCRCFAPELLLGSPSVFLFPFKPKDTLMISRTPEVTCVVDVSHEDPVPQKMYVD 123
QY      292  GVEVHNAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 351
Db      124  GVQVHNAKTKPREQQFNSTFRVSVLTVLHQWLMDGKEYCKVSNKALPAPIEKTISKTK 183
QY      352  GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 411
Db      184  GQPREPQVYTLPPSRDEMTKQVSLTCLVKGFYPSDIAVEWESSQGPENNYKTTPPMLDS 243
QY      412  DGSFFLYSKLTVDKSRWQGNVPFSCSVNHEALHNHYTQKSLSLSPG 457
Db      244  DGSFFLYSKLTVDKSRWQGNVPFSCSVNHEALHNHYTQKSLSLSPG 289

RESULT 10
I47160
Ig gamma 2b chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47160
R:KacsKovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequen
A:Reference number: I47158; MUID:95015845; PMID:7930579
A:Accession: I47160
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: EMBL:U03780; NID:g433125; PIDN:AAAS2218.1; PID:g433126
C:Genetics:
C:Gene: IgG2b
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMW>

Query Match 38.1%; Score 929.5; DB 2; Length 328;
Best Local Similarity 56.1%; Pred. No. 7.2e-52;
Matches 180; Conservative 41; Mismatches 83; Indels 17; Gaps 5

QY      143  GEKLVLNCTARTELNVGIDFNWE---YPSSHQHKLVNRDLKTQSGSEMKKFLSLTLTD 199
Db      20  GPNVALGCLASSYPPEPVTVTWNSGALTSGVHTTSPSVL-----QPSGLYSLSSMVTVP 72
QY      200  GVTRSDQGLYTCAASSGLMTKKNSTFRVRVHEKDKTHTCCPPAPPELLGSPSVFLFPFKPK 259
Db      73  ASSLSKKS-YTCNVNHPATTTKVDKRVGCTKTKPCPCIPACESP---GPSVFIPPPKPK 127
QY      260  DTLMISRTPEVTCVVDVSHEDPVPKFNWYVDGVEVHNAKTKPREQYNSTYRVVSVLTV 319
Db      128  DTLMISRTPEVTCVVDVDSQENPEVQFSWYVDGVEVHTAQRPKSEQFNSTYRVVSVLPI 187
QY      320  LHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDELTKNQVSLTCL 379
Db      188  QHQDWLNGKEYCKVSNKALPAPIRTRISKAGQREPQVYTLPPHABELSRKSVSITCL 247
QY      380  VKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQGNVPFSC 437
Db      248  VIGFYPPDIDVEWQENQPEEGNYRTTPPOQVDGTYFLYLSKFSVDKASWQGGGIFQCA 307
QY      438  VMHEALHNHYTQKSLSLSPGK 458
Db      308  VMHEALHNHYTQKSISKTGPK 328

RESULT 11
I47159
Ig gamma 2a chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47159
R:KacsKovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994

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Db 16 SMVTVPASSLSKSKS-YTCNVNHPATTTK-----VDKRVGTGKTKPCPCIPACGEGP9A 68  
QY 252 FLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 311  
Db 69 FIFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 128  
QY 312 RVSVSLTVLHQDLWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 371  
Db 129 RVSVSLPIQHDWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK 188  
QY 372 NVSLTCLLVKGFYPSDIKAVESNGQ--PENNVTTPPVLDSDGSFELYSLKLVKDSRWQ 429  
Db 189 SKVTLLCLVTFYPPDIDVQWQNGQPEPEGNRTTPPOQVDVGTFLYSKLAVDKASWQ 248  
QY 430 QGNVFSQVMHEALHNHYTKSLSPGK 458  
Db 249 RGDTFQCAVNHGALHNHYTKSLSPGK 277  
RESULT 14  
I47158  
Ig gamma 1 chain constant region - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C>Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C:Accession: I47158  
R:Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a  
A:Reference number: I47158  
A:Status: preliminary; translated from GB/EMBL/DDJ  
A:Molecule type: mRNA  
A:Residues: 1-328 <KAC>  
A:Cross-references: EMBL:U03778; NID:G433121; PIDN:AAA52216.1; PID:G433122  
C:Gene: IgG1  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:133-202/Domain: immunoglobulin homology <IMM>  
Query Match 37.5%; Score 913.5; DB 2; Length 328;  
Best Local Similarity 56.4%; Pred. No. 7.4e-51;  
Matches 181; Conservative 40; Mismatches 83; Indels 17; Gaps 6;  
QY 143 GEKLVNCTARTELNVDGIDFNWE---YPSKSHQKHLVNRDLTKTQSGSEMKKFLSTLTID 199  
Db 20 GPNVALGCLASSYFPPEVTVVNSGALTSQVHTFSPVL-----QPSGLYSLSSMTVP 72  
QY 200 GVTRSDQGLYTCASAGSLMTKNSFTVRVHEKDKHTCCPPCAPPELLGGPSVFLFPPPK 259  
Db 73 ASSLSKSKS-YTCNVNHPATTTKVDKRVGIHQ---PQCPICPCGE-VAGPSVFIFPPPK 127  
QY 260 DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVSLTV 319  
Db 128 DTLMISQTEPVTTCVVVDVSKHAEOQFSWYVDGVEVHTATREKPEQFNSTYRVSVSLPI 187  
QY 320 LHDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL 379  
Db 188 QHODMLKGEFKCKVNVNDLPAPITRTISKAIGQSRPEQVYTLPPAEELSRSKVTLTCL 247  
QY 380 VKGFYPSDIKAVESNGQ--PENNVTTPPVLDSDGSFELYSLKLVKDSRWQGNVFSK 437  
Db 248 VIGFYPPDIHVEKSNQPEPENTYRTPPQQVDGTFFLYSKLAVDKARWDHGDKECA 307  
QY 438 VMHEALHNHYTKSLSPGK 458  
Db 308 VMHEALHNHYTKSLSPGK 328  
RESULT 15  
G2GP  
Ig gamma-2 chain C region - guinea pig  
C:Species: Cavia porcellus (guinea pig)  
C>Date: 07-May-1981 #sequence\_revision 07-May-1981 #text\_change 09-Jul-2004

C:Accession: A94553; A90352; A90359; A90384; A90385; A02151  
R:Trischmann, T.M.  
submitted to the Atlas, April 1975  
A:Reference number: A94553  
A:Accession: A94553  
A:Molecule type: protein  
A:Residues: 1-3 <TRI>  
A:Cross-references: UNIPROT:P01862  
R:Birstein, B.K.; Hussain, Q.Z.; Cebra, J.J.  
Biochemistry 10, 18-25, 1971  
A:Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). III. Am  
A:Reference number: A90352; MUID:71058471; PMID:5538606  
A:Accession: A90352  
A:Molecule type: protein  
A:Residues: 4-68 <BIR>  
R:Turner, K.J.; Cebra, J.J.  
Biochemistry 10, 9-17, 1971  
A:Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II. Amir  
A:Reference number: A90359; MUID:71058486; PMID:5538616  
A:Accession: A90359  
A:Molecule type: protein  
A:Residues: 69-133:312-329 <TUR>  
R:Tracey, D.E.; Cebra, J.J.  
Biochemistry 13, 4796-4803, 1974  
A:Title: Primary structure of the C-H2 homology region from guinea pig IgG2 antibodies.  
A:Reference number: A90384; MUID:75036072; PMID:4429665  
A:Accession: A90384  
A:Molecule type: protein  
A:Residues: 134-226 <TRA>  
R:Trischmann, T.M.; Cebra, J.J.  
Biochemistry 13, 4804-4811, 1974  
A:Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibodies.  
A:Reference number: A90385; MUID:75036073; PMID:4609467  
A:Accession: A90385  
A:Molecule type: protein  
A:Residues: 227-311 <TR2>  
R:Oliveira, B.; Lamm, M.E.  
Biochemistry 10, 26-31, 1971  
A:Title: Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin.  
A:Reference number: A90354; MUID:71058474; PMID:4922544  
A:Contents: annotation; disulfide bonds  
A:Note: Cys-16 is involved in a heavy-light chain bond  
C:Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:21-81/Domain: immunoglobulin homology <IM1>  
F:135-204/Domain: immunoglobulin homology <IM2>  
F:241-310/Domain: immunoglobulin homology <IM3>  
F:28-79/Disulfide bonds: #status experimental  
F:142-202/Disulfide bonds: #status experimental  
F:178/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F:248-308/Disulfide bonds: #status experimental  
Query Match 36.9%; Score 900; DB 1; Length 329;  
Best Local Similarity 55.7%; Pred. No. 5.4e-50;  
Matches 180; Conservative 38; Mismatches 83; Indels 22; Gaps 8;  
QY 143 GEKLVNCTARTELNVDGIDFNWE---YPSKSHQKHLVNRDLTKTQSGSEMKKFLSTLTID 199  
Db 21 GSNMTLGCLVKGFPEVTVVNSGALTSQVHTFPAVL-----QSG-LYSLTSMVTVP 72  
QY 200 GVTRSDQGLYTC-AASSGLMTKNSFT--VRVHEKDKHTCCPPCAPPELLGGPSVFLFPP 256  
Db 73 SSOKA-----TCNVAHPASSTKVDKTEPIRTPEBPC-TCPCPPPELGGPSVFI 126  
QY 257 KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSV 316  
Db 127 KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSV 186  
QY 317 LTVLHQDLWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSL 376



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OM protein - protein search, using sw model

Run on: September 23, 2005, 16:57:02 ; Search time 45 Seconds  
(without alignments)  
759.762 Million cell updates/sec

Title: US-10-811-170-2

Perfect score: 2437

Sequence: 1 MVSYWDGTGVLCCALLSCLLL.....MHEALHNYTKSLSPGK 458

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:\*

1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*

2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*

3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*

4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*

5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*

6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2437	100.0	458	4	US-09-773-877B-26
2	2399	98.4	458	4	US-09-773-877B-22
3	2261	92.8	431	4	US-09-773-877B-27
4	2069.5	84.9	455	4	US-09-773-877B-24
5	2049	84.1	462	4	US-09-773-877B-18
6	2038	83.6	452	4	US-09-773-877B-16
7	2015.5	82.7	567	4	US-09-773-877B-20
8	2014.5	82.7	567	4	US-09-773-877B-12
9	2003.5	82.2	557	4	US-09-773-877B-14
10	1304	53.5	680	3	US-08-227-496C-15
11	1280	52.5	497	4	US-09-499-846-6
12	1279.5	52.5	622	4	US-09-499-846-2
13	1275.5	52.3	910	4	US-09-313-942-28
14	1274.5	52.3	525	4	US-09-499-846-4
15	1269.5	52.1	488	4	US-09-499-846-12
16	1269	52.1	388	3	US-09-131-247-16
17	1269	52.1	388	4	US-09-784-623-16
18	1265	51.9	347	1	US-07-940-861-43
19	1265	51.9	347	1	US-08-459-512-43
20	1265	51.9	347	2	US-08-459-657-43
21	1265	51.9	347	2	US-08-460-132-43
22	1265	51.9	347	3	US-08-466-465-8
23	1265	51.9	347	4	US-09-730-465-8
24	1265	51.9	347	5	PCT-US92-02050-43
25	1265	51.9	497	4	US-09-499-846-10
26	1261	51.7	459	1	US-08-157-101A-7
27	1259.5	51.7	525	4	US-09-499-846-8

Sequence 25, Appl  
Sequence 54, Appl  
Sequence 53, Appl  
Sequence 20, Appl  
Sequence 22, Appl  
Sequence 4, Appl  
Sequence 11, Appl  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 248, Appl  
Sequence 42, Appl  
Sequence 210, Appl  
Sequence 222, Appl  
Sequence 224, Appl  
Sequence 228, Appl  
Sequence 238, Appl  
Sequence 240, Appl  
Sequence 242, Appl

ALIGNMENTS

RESULT 1

US-09-773-877B-26  
; Sequence 26, Application US/09773877B  
; Patent No. 6833349  
; GENERAL INFORMATION:  
; APPLICANT: Xia, Yu-Ping et al.  
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES  
; FILE REFERENCE: REG 710b  
; CURRENT APPLICATION NUMBER: US/09/773,877B  
; CURRENT FILING DATE: 2001-01-31  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 26  
; LENGTH: 458  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: VEGPR1R2-FcdeltaCl(a) Receptor  
; US-09-773-877B-26

Query Match	100.0%;	Score 2437;	DB 4;	Length 458;
Best Local Similarity	100.0%;	Pred. No. 1.3e-196;		
Matches	458;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
Qy	1	MVSYWDGTGVLCCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIHHMTEGRELVI	PCRVTS	60
Db	1	MVSYWDGTGVLCCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIHHMTEGRELVI	PCRVTS	60
Qy	61	PNITVTLLKKPLDPLIPDGKRIIWDNRKGFIIISNATYKEIGLLTCEATVNGHLYKT	NYLT	120
Db	61	PNITVTLLKKPLDPLIPDGKRIIWDNRKGFIIISNATYKEIGLLTCEATVNGHLYKT	NYLT	120
Qy	121	HROTNTIIDVLSPSGIELSVGEKLVNCTARTELNVGIDFNWYESSKHQHKLVNRD	180	
Db	121	HROTNTIIDVLSPSGIELSVGEKLVNCTARTELNVGIDFNWYESSKHQHKLVNRD	180	
Qy	181	LKTQSGEMKKFSLTLLIDGVTRSDQGLYTCASSGLMTKKNSTFVRVHEKDKHTHT	CPCC	240
Db	181	LKTQSGEMKKFSLTLLIDGVTRSDQGLYTCASSGLMTKKNSTFVRVHEKDKHTHT	CPCC	240
Qy	241	PAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA	KT	300
Db	241	PAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA	KT	300
Qy	301	KPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSKNALKAPAEKTIISKAKGPQRPQVY	360	
Db	301	KPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSKNALKAPAEKTIISKAKGPQRPQVY	360	
Qy	361	TLPPSRDELTKNOVSLTCLVKGYFSPDAVWEWSNGKPPENNYKTTPPVLSDGSGF	FLYSK	420
Db	361	TLPPSRDELTKNOVSLTCLVKGYFSPDAVWEWSNGKPPENNYKTTPPVLSDGSGF	FLYSK	420

Db 361 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 420  
QY 421 LTVDKSRWQGNVPSVCSVMHEALHNHYTQKSLSLSPGK 458  
Db 421 LTVDKSRWQGNVPSVCSVMHEALHNHYTQKSLSLSPGK 458  
RESULT 2  
US-09-773-877B-22  
; Sequence 22, Application US/09773877B  
; Patent No. 6833349  
; GENERAL INFORMATION:  
; APPLICANT: Xia, Yu-Ping et al.  
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES  
; FILE REFERENCE: REG 710b  
; CURRENT APPLICATION NUMBER: US/09/773,877B  
; CURRENT FILING DATE: 2001-01-31  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 22  
; LENGTH: 458  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: FcId2.FcId3.FcIdtaC1(a) Receptor  
US-09-773-877B-22

Query Match 98.4%; Score 2399; DB 4; Length 458;  
Best Local Similarity 98.7%; Pred. No. 2e-193;  
Matches 455; Conservative 0; Mismatches 0; Indels 6; Gaps 2;  
QY 1 MVSYPDVTGVLCCALLSCLLLTGSSGSDTCGRPFVEMYSEIPEIHHMTEGRELVIPCRVTS 60  
Db 1 MVSYPDVTGVLCCALLSCLLLTGSSG---GRPFVEMYSEIPEIHHMTEGRELVIPCRVTS 57  
QY 61 PNITVTLLKPEPLDTLPDGKRIIWDNRKGFIIISNATYKEIGLLTCEATVNGHLYKTNLYT 120  
Db 58 PNITVTLLKPEPLDTLPDGKRIIWDNRKGFIIISNATYKEIGLLTCEATVNGHLYKTNLYT 117  
QY 121 HRQNTIIDVVLSPSHGIELSVGEKLVNCTARTELNVGIDFNWYPSKHKHKLNVNRD 180  
Db 118 HRQNTIIDVVLSPSHGIELSVGEKLVNCTARTELNVGIDFNWYPSKHKHKLNVNRD 177  
QY 181 LKTSQSEMCKFLSTLTIDGVTRSDQGLYTCASSGLMTKKNSTFVRVHEK---DKHTC 237  
Db 178 LKTSQSEMCKFLSTLTIDGVTRSDQGLYTCASSGLMTKKNSTFVRVHEKGPDKHTC 237  
QY 238 PPCPAPELLGGPSVFLFPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 297  
Db 238 PPCPAPELLGGPSVFLFPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 297  
QY 298 AKTKPREEQNSTYRVVSVLTVLHQDLWLNKYEKCKVSNKALPAPIEKTISKAKGQPREP 357  
Db 298 AKTKPREEQNSTYRVVSVLTVLHQDLWLNKYEKCKVSNKALPAPIEKTISKAKGQPREP 357  
QY 358 QVTLPSPRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 417  
Db 358 QVTLPSPRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 417  
QY 418 YSKLTVDKSRWQGNVPSVCSVMHEALHNHYTQKSLSLSPGK 458  
Db 418 YSKLTVDKSRWQGNVPSVCSVMHEALHNHYTQKSLSLSPGK 458

RESULT 3  
US-09-773-877B-27  
; Sequence 27, Application US/09773877B  
; Patent No. 6833349  
; GENERAL INFORMATION:  
; APPLICANT: Xia, Yu-Ping et al.  
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES  
; FILE REFERENCE: REG 710b  
; CURRENT APPLICATION NUMBER: US/09/773,877B

; CURRENT FILING DATE: 2001-01-31  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 27  
; LENGTH: 431  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Peptide  
US-09-773-877B-27

Query Match 92.8%; Score 2261; DB 4; Length 431;  
Best Local Similarity 99.1%; Pred. No. 7.5e-182;  
Matches 428; Conservative 0; Mismatches 0; Indels 4; Gaps 2;  
QY 30 GRPFVEMYSEIPEIHHMTEGRELVIPCRVTSPTNITVTLKKFPDLDTLPDGKRIIWDNRK 89  
Db 1 GRPFVEMYSEIPEIHHMTEGRELVIPCRVTSPTNITVTLKKFPDLDTLPDGKRIIWDNRK 60  
QY 90 FIISNATYKEIGLLTCEATVNGHLYKTNLYTHRQNTIIDVVLSPSHGIELSVGEKLVN 149  
Db 61 FIISNATYKEIGLLTCEATVNGHLYKTNLYTHRQNTIIDVVLSPSHGIELSVGEKLVN 120  
QY 150 CTARTELNVGIDFNWYPSKHKHKLNVNRDLKTSQSEMCKFLSTLTIDGVTRSDQGLY 209  
Db 121 CTARTELNVGIDFNWYPSKHKHKLNVNRDLKTSQSEMCKFLSTLTIDGVTRSDQGLY 180  
QY 210 TCAASSGLMTKKNSTFVRVHEK---DKHTCPCPAPELLGGPSVFLFPPPKPDTLMISR 266  
Db 181 TCAASSGLMTKKNSTFVRVHEKGPDKHTCPCPAPELLGGPSVFLFPPPKPDTLMISR 240  
QY 267 TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQNSTYRVVSVLTVLHQDLN 326  
Db 241 TPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQNSTYRVVSVLTVLHQDLN 300  
QY 327 GREYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDELTKNQVSLTCLVKGFYPS 386  
Db 301 GREYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDELTKNQVSLTCLVKGFYPS 359  
QY 387 DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQGNVPSVCSVMHEALHNH 446  
Db 360 DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQGNVPSVCSVMHEALHNH 419  
QY 447 YTKSLSLSPGK 458  
Db 420 YTKSLSLSPGK 431

RESULT 4  
US-09-773-877B-24  
; Sequence 24, Application US/09773877B  
; Patent No. 6833349  
; GENERAL INFORMATION:  
; APPLICANT: Xia, Yu-Ping et al.  
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES  
; FILE REFERENCE: REG 710b  
; CURRENT APPLICATION NUMBER: US/09/773,877B  
; CURRENT FILING DATE: 2001-01-31  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 24  
; LENGTH: 455  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: FcId2.VEGFR3D3.FcIdtaC1(a) Receptor  
US-09-773-877B-24

Query Match 84.9%; Score 2069.5; DB 4; Length 455;  
Best Local Similarity 85.7%; Pred. No. 1e-165;  
Matches 395; Conservative 16; Mismatches 41; Indels 9; Gaps 3;  
QY 1 MVSYPDVTGVLCCALLSCLLLTGSSGSDTCGRPFVEMYSEIPEIHHMTEGRELVIPCRVTS 60

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Db 1 MVSWDTGVLCCALLTGSSG---GRPFVEMYSEIPEIIMHTEGRELVI PCRVTS 57
Qy 61 PNITVTLKKFPDLTLPDGKRIIWDNRKGFIIISNATYKEIGLLTCEATVNGHLYKTNLT 120
Db 58 PNITVTLKKFPDLTLPDGKRIIWDNRKGFIIISNATYKEIGLLTCEATVNGHLYKTNLT 117
Qy 121 HRQNTIIVVLSHGIELSVGEKLVNCTARTELNVGIDFNWYPSKHQHKLVNRD 180
Db 118 HRQNTIIVVLSHGIELSVGEKLVNCTARTELNVGIDFNWYPSKHQHKLVNRD 177
Qy 181 LKQSGEMKKFLSTLTIDGVTSDQGLYTCASSGLMTKKNSTFVRVHEK---DKHTHC 237
Db 178 RSQQTHTELS---SILTIHNVSDHGLSYVCKANNGIQRPRESTEVIVHENGPGDKTHC 234
Qy 238 PPCPAPELLGGPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGEVHN 297
Db 235 PPCPAPELLGGPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGEVHN 294
Qy 298 AKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 357
Db 295 AKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 354
Qy 358 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFLL 417
Db 355 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFLL 414
Qy 418 YSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 458
Db 415 YSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 455

RESULT 5
US-09-773-877B-18
; Sequence 18, Application US/09773877B
; Patent No. 6833349
; GENERAL INFORMATION:
; APPLICANT: Xia, Yu-Ping et al.
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
; FILE REFERENCE: REG 710b
; CURRENT APPLICATION NUMBER: US/09/773, 877B
; CURRENT FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Flt1(2-3)-Fc (Mut3)
US-09-773-877B-18

Query Match 84.1%; Score 2049; DB 4; Length 462;
Best Local Similarity 84.2%; Pred. No. 5.6e-164;
Matches 393; Conservative 13; Mismatches 47; Indels 14; Gaps 3;

Qy 1 MVSWDTGVLCCALLTGSSGSDTGRPFVEMYSEIPEIIMHTEGRELVI PCRVTS 60
Db 1 MVSWDTGVLCCALLTGSSGSDTGRPFVEMYSEIPEIIMHTEGRELVI PCRVTS 57
Qy 61 PNITVTLKKFPDLTLPDGKRIIWDNRKGFIIISNATYKEIGLLTCEATVNGHLYKTNLT 120
Db 58 PNITVTLKKFPDLTLPDGKRIIWDNRKGFIIISNATYKEIGLLTCEATVNGHLYKTNLT 117
Qy 121 HRQNTIIVVLSHGIELSVGEKLVNCTARTELNVGIDFNWYPSKHQHKLVNRD 180
Db 118 HRQNTIIVVLSHGIELSVGEKLVNCTARTELNVGIDFNWYPSKHQHKLVNRD 176
Qy 181 LKQSGEMKKFLSTLTIDGVTSDQGLYTCASSGLMTKKNSTFVRVHEK-----231
Db 177 -IDQSNHANIFYSVLTIIDKQNKDKGLYTCRVSRGPFKSVNTSVHIYDKAGGEPKSC 235
Qy 232 DKHTHTCPCPAPELLGGPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYD 291
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Db 236 DKHTHTCPCPAPELLGGPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYD 295
Qy 292 GVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 351
Db 296 GVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 355
Qy 352 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 411
Db 356 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 415
Qy 412 DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 458
Db 416 DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 462

RESULT 6
US-09-773-877B-16
; Sequence 16, Application US/09773877B
; Patent No. 6833349
; GENERAL INFORMATION:
; APPLICANT: Xia, Yu-Ping et al.
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
; FILE REFERENCE: REG 710b
; CURRENT APPLICATION NUMBER: US/09/773, 877B
; CURRENT FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Flt1(2-3 deltaB) -Fc
US-09-773-877B-16

Query Match 83.6%; Score 2038; DB 4; Length 452;
Best Local Similarity 83.9%; Pred. No. 4.6e-163;
Matches 392; Conservative 10; Mismatches 41; Indels 24; Gaps 3;

Qy 1 MVSWDTGVLCCALLTGSSGSDTGRPFVEMYSEIPEIIMHTEGRELVI PCRVTS 60
Db 1 MVSWDTGVLCCALLTGSSGSDTGRPFVEMYSEIPEIIMHTEGRELVI PCRVTS 57
Qy 61 PNITVTLKKFPDLTLPDGKRIIWDNRKGFIIISNATYKEIGLLTCEATVNGHLYKTNLT 120
Db 58 PNITVTLKKFPDLTLPDGKRIIWDNRKGFIIISNATYKEIGLLTCEATVNGHLYKTNLT 117
Qy 121 HRQNTIIVVLSHGIELSVGEKLVNCTARTELNVGIDFNWYPSKHQHKLVNRD 180
Db 118 HRQNTIIVVLSHGIELSVGEKLVNCTARTELNVGIDFNWYPSKHQHKLVNRD 165
Qy 181 LKQSGEMKKFLSTLTIDGVTSDQGLYTCASSGLMTKKNSTFVRVHEK-----231
Db 166 EIDQSNHANIFYSVLTIIDKQNKDKGLYTCRVSRGPFKSVNTSVHIYDKAGGEPKSC 225
Qy 232 DKHTHTCPCPAPELLGGPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYD 291
Db 226 DKHTHTCPCPAPELLGGPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWYD 285
Qy 292 GVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 351
Db 286 GVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 345
Qy 352 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 411
Db 346 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 405
Qy 412 DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 458
Db 406 DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 452
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## RESULT 7

US-09-773-877B-20  
; Sequence 20, Application US/09773877B  
; Patent No. 6833349  
; GENERAL INFORMATION:  
; APPLICANT: Xia, Yu-Ping et al.  
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES  
; FILE REFERENCE: REG 710b  
; CURRENT APPLICATION NUMBER: US/09/773,877B  
; CURRENT FILING DATE: 2001-01-31  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 20  
; LENGTH: 567  
; TYPE: PR1  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: F1t1(1-3 R->N)-Fc (Mut4)  
US-09-773-877B-20

Query Match 82.7%; Score 2015.5; DB 4; Length 567;  
Best Local Similarity 69.6%; Pred. No. 4.9e-161;  
Matches 396; Conservative 14; Mismatches 46; Indels 113; Gaps 3;

QY	1	MVSYWDTGVLLCALLSCLLLTGSSSG-----	26
Db	1	MVSYWDTGVLLCALLSCLLLTGSSSGKLDPELSLKGTHIMQAGTTLHLCRGEAAHK	60
QY	27	-----	26
Db	61	WSPLEMVSKESERLSITKSACGRNGKQFCSTLTNTAQAANHTGYFCKYLAVPTSKKET	120
QY	27	-----SDTGRPFVEMYSEIPEIIHMTGRELVIPCRVTSPNITVTLLKKFPLDLTLPD	78
Db	121	ESAIYIFISDTGRPFVEMYSEIPEIIHMTGRELVIPCRVTSPNITVTLLKKFPLDLTLPD	180
QY	79	GKRIIWDNRKGFIIISNATYKEIGLLTCEATVNGHLYKTNVLTHTROQNTIIDVLSPSHGI	138
Db	181	GKRIIWDNRKGFIIISNATYKEIGLLTCEATVNGHLYKTNVLTHTROQNTIIDVQISTPRPV	240
QY	139	ELSVGKLVNCTARTELNVGIDFNWEYPSSKHQKKLVNRDLKTQSGEMKKFLSTLTI	198
Db	241	KLLRGHTLVNCTATTPLNTRVQMTWSYPDEKNKASVRRR--IDQSNHANIFYSVLTI	298
QY	199	DGVTSDQGLYTCAASGLMTKKNSTFVRVHEK-----DKHTCCPCPAPELLGGP	249
Db	299	DKMQNKDGLYTCRVRSGPSFKSVNTSVHIYDKAGPEPKSCDKHTCCPCPAPELLGGP	358
QY	250	SVFLFPKPKDITLMIISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYNS	309
Db	359	SVFLFPKPKDITLMIISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYNS	418
QY	310	TYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDEL	369
Db	419	TYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDEL	478
QY	370	TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDKSRWQ	429
Db	479	TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDKSRWQ	538
QY	430	QGNVFSCSVNHEALHNHYTQKSLSLSPGK	458
Db	539	QGNVFSCSVNHEALHNHYTQKSLSLSPGK	567

## RESULT 8

US-09-773-877B-12  
; Sequence 12, Application US/09773877B  
; Patent No. 6833349  
; GENERAL INFORMATION:  
; APPLICANT: Xia, Yu-Ping et al.  
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES  
; FILE REFERENCE: REG 710b

; CURRENT APPLICATION NUMBER: US/09/773,877B  
; CURRENT FILING DATE: 2001-01-31  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 12  
; LENGTH: 567  
; TYPE: PR1  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: F1t(1-3)-Fc  
US-09-773-877B-12

Query Match 82.7%; Score 2014.5; DB 4; Length 567;  
Best Local Similarity 69.6%; Pred. No. 6e-161;  
Matches 396; Conservative 13; Mismatches 47; Indels 113; Gaps 3;

QY	1	MVSYWDTGVLLCALLSCLLLTGSSSG-----	26
Db	1	MVSYWDTGVLLCALLSCLLLTGSSSGKLDPELSLKGTHIMQAGTTLHLCRGEAAHK	60
QY	27	-----	26
Db	61	WSPLEMVSKESERLSITKSACGRNGKQFCSTLTNTAQAANHTGYFCKYLAVPTSKKET	120
QY	27	-----SDTGRPFVEMYSEIPEIIHMTGRELVIPCRVTSPNITVTLLKKFPLDLTLPD	78
Db	121	ESAIYIFISDTGRPFVEMYSEIPEIIHMTGRELVIPCRVTSPNITVTLLKKFPLDLTLPD	180
QY	79	GKRIIWDNRKGFIIISNATYKEIGLLTCEATVNGHLYKTNVLTHTROQNTIIDVLSPSHGI	138
Db	181	GKRIIWDNRKGFIIISNATYKEIGLLTCEATVNGHLYKTNVLTHTROQNTIIDVQISTPRPV	240
QY	139	ELSVGKLVNCTARTELNVGIDFNWEYPSSKHQKKLVNRDLKTQSGEMKKFLSTLTI	198
Db	241	KLLRGHTLVNCTATTPLNTRVQMTWSYPDEKNKASVRRR--IDQSNHANIFYSVLTI	298
QY	199	DGVTSDQGLYTCAASGLMTKKNSTFVRVHEK-----DKHTCCPCPAPELLGGP	249
Db	299	DKMQNKDGLYTCRVRSGPSFKSVNTSVHIYDKAGPEPKSCDKHTCCPCPAPELLGGP	358
QY	250	SVFLFPKPKDITLMIISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYNS	309
Db	359	SVFLFPKPKDITLMIISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQYNS	418
QY	310	TYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDEL	369
Db	419	TYRVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRDEL	478
QY	370	TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDKSRWQ	429
Db	479	TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDKSRWQ	538
QY	430	QGNVFSCSVNHEALHNHYTQKSLSLSPGK	458
Db	539	QGNVFSCSVNHEALHNHYTQKSLSLSPGK	567

## RESULT 9

US-09-773-877B-14  
; Sequence 14, Application US/09773877B  
; Patent No. 6833349  
; GENERAL INFORMATION:  
; APPLICANT: Xia, Yu-Ping et al.  
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES  
; FILE REFERENCE: REG 710b  
; CURRENT APPLICATION NUMBER: US/09/773,877B  
; CURRENT FILING DATE: 2001-01-31  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 14  
; LENGTH: 557  
; TYPE: PR1  
; ORGANISM: Artificial Sequence



FEATURE:  
OTHER INFORMATION: Flt1(1-3 deltaB)-Fc (Mut1)  
US-09-773-877B-14

Query Match 82.2%; Score 2003.5; DB 4; Length 557;  
Best Local Similarity 69.4%; Pred. No. 4.9e-160;  
Matches 395; Conservative 10; Mismatches 41; Indels 123; Gaps 3;

QY 1 MVS YWDTGVLLCALLSCLLLTGSSG-----26  
DB 1 MVS YWDTGVLLCALLSCLLLTGSSGSKLDPKLSLKGTHMQAGQTLHLQCRGEAAHK 60  
QY 27 -----26  
DB 61 WSLPVMVSKESERLSITKACGRNGKQFCSTLTNTAQANHGTGYSKYLAVPTSKKET 120  
QY 27 -----SDTGRPFVEMVSEIPEIIMHTEGRELVI PCRVTSNITVTLKKPFLDLTLPD 78  
DB 121 ESAIYIFISDTGRPFVEMVSEIPEIIMHTEGRELVI PCRVTSNITVTLKKPFLDLTLPD 180  
QY 79 GKRIIWDNRKGFIIISNATYKEIGLLTCEATVNGHLKYNTYLTHRQNTIIDVVLSPSHGI 138  
DB 181 GKRIIWDNRKGFIIISNATYKEIGLLTCEATVNGHLKYNTYLTHRQNTIIDVQISTPRPV 240  
QY 139 ELSVGEKLVNCTARTLVNIGIDFNWEPSSKHOKKLVNRDLKTSQSGEMKKFLSTLT 198  
DB 241 KLLRGHTLVNCTATTPLNTRVQMTSYP-----DEIDQSNHANIFYSVLTI 288  
QY 199 DGVTSDQGLYTCAASGLMTKNGSTFVRVHEK-----DKTHTCPCPAPPELLGGP 249  
DB 289 DKMQNKDKGLYTCRVSRGSPFSKSVNTSVHIYKAGPCKSCDKTHTCPCPAPPELLGGP 348  
QY 250 SVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVEVHNATKPREOYNS 309  
DB 349 SVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVEVHNATKPREOYNS 408  
QY 310 TYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKQPREPOVYTLPPSRDEL 369  
DB 409 TYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKQPREPOVYTLPPSRDEL 468  
QY 370 TKQVSLTCLVKGFYPSDIAVEWESNGQPNYKTPPVLDSDGSPFLYSKLTVDKSRWQ 429  
DB 469 TKQVSLTCLVKGFYPSDIAVEWESNGQPNYKTPPVLDSDGSPFLYSKLTVDKSRWQ 528  
QY 430 QGNVFCVSNVHEALHNHYTKSLSPGK 458  
DB 529 QGNVFCVSNVHEALHNHYTKSLSPGK 557

RESULT 10  
US-08-227-496C-15  
Sequence 15, Application US/08227496C  
Patent No. 6130202  
GENERAL INFORMATION:  
APPLICANT: Greve, Jeffrey M.  
APPLICANT: McClelland, Alan  
TITLE OF INVENTION: Multimeric Forms of Human  
TITLE OF INVENTION: Rhinovirus Receptor Protein  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Bayer Corporation  
STREET: 400 Morgan Lane  
CITY: West Haven  
STATE: Connecticut  
COUNTRY: USA  
ZIP: 06516  
COMPUTER READABLE FORM:  
MEDIUM TYPE: diskette, 1.44 Mb storage  
COMPUTER: Dell Optiplex GX1  
OPERATING SYSTEM: Windows 95  
SOFTWARE: WordPerfect 8.0 for Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/227,496C

FILING DATE: 04/14/94  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/903,069  
FILING DATE: 06/22/92  
APPLICATION NUMBER: 07/704,984  
FILING DATE: 05/24/91  
APPLICATION NUMBER: 07/556,238  
FILING DATE: 07/20/90  
ATTORNEY/AGENT INFORMATION:  
NAME: Barbara A. Shimei  
REGISTRATION NUMBER: 29,862  
REFERENCE/DOCKET NUMBER: MTI 214.2C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (203) 812-2786  
TELEFAX: (203) 812-5492  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 680 amino acid residues  
TYPE: amino acids  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
DESCRIPTION: protein  
HYPOTHEICAL: no  
FRAGMENT TYPE: complete sequence  
FEATURE:  
NAME/KEY: tICAM(185)/IgG fusion protein  
OTHER INFORMATION: amino acid residues 1-453 =  
OTHER INFORMATION: tICAM(453); amino acid residues 454-680 = amino  
OTHER INFORMATION: acid residues 216-442 of human IgG1 heavy chain  
US-08-227-496C-15

Query Match 53.5%; Score 1304; DB 3; Length 680;  
Best Local Similarity 60.6%; Pred. No. 4.4e-101;  
Matches 281; Conservative 30; Mismatches 89; Indels 64; Gaps 15;

QY 15 LSCLLLTSSGSDTGRPFVEMYS-EIPRII-----HMTGRELVI PCRVTSNITVTLKK 69  
DB 261 LTCVILGNQSETL--QVTIYSPAPNVILTKPEVSEGTETVACE-AHPRAKVTLNG 317  
QY 70 FLDTLIPGKRIIWDNRKGFIIISNATYKEIG--LLTCEATVNGHLKYNTYLTHRQNTII 128  
DB 318 VPAQPLGP-----RAQLLKATPEDNCRSFSCSAT----LEVAQQLIHKNOTREL 363  
QY 129 DVVLSPSHGIELSVGEKLVNCTARTLVNIGIDFNWEPSSKHOKKLVNRDLKTSQSGE 108  
DB 364 RVLYGP-----RLDER---DCPG-----NMTWPNSSQTP-----MCQAWGN 397  
QY 189 MKKFLSTLTIDG-----VTRSDQGLYTCAASS--GLMTKKNSTFV-EVHEKDKT 234  
DB 398 PLPELKCLK-DGTFPLPIGESVTITRDLGTYLCRARSTQGEVTRKVTNVLSPRYEDKT 456  
QY 235 HTCPCPAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVE 294  
DB 457 HTCPCPAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVE 516  
QY 295 VHNATKPREOYNSYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKQOP 354  
DB 517 VHNATKPREOYNSYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKQOP 576  
QY 355 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPNYKTPPVLDSDGS 414  
DB 577 REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPNYKTPPVLDSDGS 636  
QY 415 FFYLSKLTVDKSRWQGNVFCVSNVHEALHNHYTKSLSPGK 458  
DB 637 FFYLSKLTVDKSRWQGNVFCVSNVHEALHNHYTKSLSPGK 680

RESULT 11  
US-09-499-846-6  
Sequence 6, Application US/09499846  
Patent No. 6656728

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; GENERAL INFORMATION:
; APPLICANT: Kavanaugh et al.
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR
; FILE REFERENCE: 035784/195012 (5784-
; CURRENT APPLICATION NUMBER: US/09/499,846
; CURRENT FILING DATE: 2000-02-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-499-846-6

Query Match      52.5%; Score 1280; DB 4; Length 497;
Best Local Similarity 54.3%; Pred. No. 2.9e-99;
Matches 284; Conservative 32; Mismatches 109; Indels 98; Gaps 12;

QY 5 WDTGVLLCALLSLCLLTGSSSGSDTGRPPFVEMYSEIP-----GLLTC 105
Db 5 WDTGVLLCALLSLCLLTGSSSGSDTGRPPFVEMYSEIP-----GLLTC 105
QY 60 -----SPNITVTLKKFPLDILPDKRIIWDNR-KGFIISNATYKEI----- 111
Db 60 PSSGTPNPLRWLK-----NGKEFKPDHRIIGGYKRYATWSIIMDSVPSDKGNYTC 111
QY 106 -----BATVNGHLYKTNLYTHROTNTIIDVLSPSHGIELSVGEKVLNCTARTLNVTG 160
Db 112 IVENEYGSIN-HTYQ-----LDVVERSPHRPILQAG-----LPANKTVALGSNV 154
QY 161 DFNWEYPSSKHQHKLVN-----RDLTQSGSEMKKFLSTLTIDGVT 203
Db 155 EFCKYVSDPQPHIOWLKHIEVNGSKIGPDNLPYVQILKTAGVNTTDMKEMVLHLENVSF 214
QY 204 SDOGLYTCASSGLMTKKNSTFVRVHEK-----DKTH 235
Db 215 EDAGEYTCLAGNSIGLSHSAWLTIVLEALEERPAVMTSPLYLEGSGLQEPKSCDKTH 274
QY 236 TCPCPAPPELLGGPSVFLPFPKPTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEV 295
Db 275 TCPCPAPPELLGGPSVFLPFPKPTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEV 334
QY 296 HNAKTPREOYNSTYRVVSVLTVLHDQDLWGKGYCKVSNKALPAPIEKTISKAKGQPR 355
Db 335 HNAKTPREOYNSTYRVVSVLTVLHDQDLWGKGYCKVSNKALPAPIEKTISKAKGQPR 394
QY 356 EPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 415
Db 395 EQOYVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 454
QY 416 FLYSKLTVDKSRWQOQGNVFSVCSVMHEALHNHYTQKSLSLSPGK 458
Db 455 FLYSKLTVDKSRWQOQGNVFSVCSVMHEALHNHYTQKSLSLSPGK 497

RESULT 12
US-09-499-846-2
; Sequence 2, Application US/09499846
; Patent No. 6656728
; GENERAL INFORMATION:
; APPLICANT: Kavanaugh et al.
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR
; FILE REFERENCE: 035784/195012 (5784-
; CURRENT APPLICATION NUMBER: US/09/499,846
; CURRENT FILING DATE: 2000-02-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 622
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-499-846-2
; Sequence 28, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
; TITLE OF INVENTION: AND USING
; FILE REFERENCE: REG 203-A
; CURRENT APPLICATION NUMBER: US/09/313,942
; CURRENT FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 09/313,942
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: 60/101,858
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 910
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-313-942-28

Query Match      52.3%; Score 1275.5; DB 4; Length 910;
Best Local Similarity 63.5%; Pred. No. 1.7e-98;
Matches 257; Conservative 42; Mismatches 77; Indels 29; Gaps 9;
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Search completed: September 23, 2005, 17:18:51  
Job time : 48 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 23, 2005, 17:12:57 ; Search time 123 Seconds  
(without alignments)  
1515,541 Million cell updates/sec

Title: US-10-811-170-2

Perfect score: 2437

Sequence: 1 MVSYWDGTGVLCCALLSCLLL.....MHEALHNYTKSLSPGK 458

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1826521 seqs, 407012169 residues

Total number of hits satisfying chosen parameters: 1826521

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Published Applications AA:\*

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- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
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- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09H\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US10E\_PUBCOMB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US11A\_PUBCOMB.pep.\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
- 21: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2437	100.0	458	10	US-09-773-877A-26
2	2437	100.0	458	15	US-10-609-775-10
3	2437	100.0	458	16	US-10-860-958-2
4	2437	100.0	458	17	US-10-830-902-2
5	2437	100.0	458	17	US-10-897-802-2
6	2437	100.0	458	17	US-10-880-021-10
7	2437	100.0	458	17	US-10-909-011-4
8	2437	100.0	458	18	US-10-988-243-16
9	2437	100.0	458	18	US-10-998-881-4
10	2437	100.0	458	20	US-11-016-097-16
11	2437	100.0	458	20	US-11-039-144-2

12	2399	98.4	458	10	US-09-773-877A-22	Sequence 22, Appl
13	2399	98.4	458	15	US-10-609-775-8	Sequence 8, Appl
14	2399	98.4	458	17	US-10-880-021-8	Sequence 8, Appl
15	2399	98.4	458	17	US-10-909-011-2	Sequence 2, Appl
16	2399	98.4	458	18	US-10-988-243-12	Sequence 12, Appl
17	2399	98.4	458	18	US-10-998-881-2	Sequence 2, Appl
18	2399	98.4	458	20	US-11-016-097-12	Sequence 12, Appl
19	2399	98.4	458	20	US-11-016-097-12	Sequence 12, Appl
20	2399	98.4	458	20	US-11-016-097-12	Sequence 12, Appl
21	2261	92.6	431	10	US-09-773-877A-27	Sequence 27, Appl
22	2261	92.6	431	10	US-09-773-877A-27	Sequence 27, Appl
23	2256.5	92.6	430	20	US-11-016-097-17	Sequence 17, Appl
24	2256.5	92.6	430	20	US-11-016-097-17	Sequence 17, Appl
25	2069.5	84.9	455	10	US-09-773-877A-24	Sequence 24, Appl
26	2069.5	84.9	455	17	US-10-609-775-13	Sequence 13, Appl
27	2069.5	84.9	455	17	US-10-880-021-13	Sequence 13, Appl
28	2069.5	84.9	455	18	US-10-988-243-14	Sequence 14, Appl
29	2069.5	84.9	455	20	US-11-016-097-14	Sequence 14, Appl
30	2049	84.1	462	10	US-09-773-877A-18	Sequence 18, Appl
31	2049	84.1	462	18	US-10-988-243-8	Sequence 8, Appl
32	2038	83.6	452	10	US-09-773-877A-16	Sequence 16, Appl
33	2038	83.6	452	18	US-10-988-243-6	Sequence 6, Appl
34	2038	83.6	452	20	US-11-016-097-6	Sequence 6, Appl
35	2015.5	82.7	567	10	US-09-773-877A-20	Sequence 20, Appl
36	2015.5	82.7	567	18	US-10-988-243-10	Sequence 10, Appl
37	2015.5	82.7	567	20	US-11-016-097-10	Sequence 10, Appl
38	2014.5	82.7	567	10	US-09-773-877A-12	Sequence 12, Appl
39	2014.5	82.7	567	18	US-10-988-243-2	Sequence 2, Appl
40	2014.5	82.7	567	20	US-11-016-097-2	Sequence 2, Appl
41	2003.5	82.2	557	10	US-09-773-877A-14	Sequence 14, Appl
42	2003.5	82.2	557	18	US-10-988-243-4	Sequence 4, Appl
43	2003.5	82.2	557	20	US-11-016-097-4	Sequence 4, Appl
44	1726.5	70.8	934	14	US-10-232-838-17	Sequence 17, Appl
45	1716	70.4	949	14	US-10-232-838-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1

US-09-773-877A-26  
; Sequence 26, Application US/09773877A  
; Publication No. US20030017977A1  
; GENERAL INFORMATION:  
; APPLICANT: Xia, Yu-Ping et al.  
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES  
; FILE REFERENCE: REG 710b  
; CURRENT APPLICATION NUMBER: US/09/773,877A  
; CURRENT FILING DATE: 2001-01-31  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 26  
; LENGTH: 458  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: VEGFR1R2-FcdeltaC1(a) Receptor  
US-09-773-877A-26

Query Match 100.0%; Score 2437; DB 10; Length 458;  
Best Local Similarity 100.0%; Pred. No. 3.5e-152;  
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MVSYWDGTGVLCCALLSCLLLTSSGSDTGRPPVEMYSEIPEIHHMTEGRELVIPCRVTS	60
Db	1	MVSYWDGTGVLCCALLSCLLLTSSGSDTGRPPVEMYSEIPEIHHMTEGRELVIPCRVTS	60
Qy	61	PNITVTLKFPDLTLPDGKRIIWDNRKGFIIISNATYKEIGLTTCBATVNGHLYKTNLT	120
Db	61	PNITVTLKFPDLTLPDGKRIIWDNRKGFIIISNATYKEIGLTTCBATVNGHLYKTNLT	120
Qy	121	HRQTNTIIVLSPSHGIELSVGEKLVLCNTARTLNVGIDFNWEYPSKHQHKLVNRD	180

Db 121 HROTNTIIDVVLSPSHGIELSVGEKLVNCTARTELNVGIDFNWVEYPSKQHKKLVNRD 180  
Qy 181 LKQSGSEMMKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKDKHTHTCPPC 240  
Db 181 LKQSGSEMMKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKDKHTHTCPPC 240  
Qy 241 PAPELLGGPSVFLFPKPKDTLMISTRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 300  
Db 241 PAPELLGGPSVFLFPKPKDTLMISTRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 300  
Qy 301 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 360  
Db 301 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 360  
Qy 361 TLPPSRDELTKNQVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSK 420  
Db 361 TLPPSRDELTKNQVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSK 420  
Qy 421 LTVDKSRWQOQGNVFCSCVMHEALHNNHYTQKSLSLSPGK 458  
Db 421 LTVDKSRWQOQGNVFCSCVMHEALHNNHYTQKSLSLSPGK 458

## RESULT 2

US-10-609-775-10  
; Sequence 10, Application US/10609775  
; Publication No. US20040014667A1  
; GENERAL INFORMATION:  
; APPLICANT: Thomas J. Daly  
; APPLICANT: James P. Fandl  
; APPLICANT: Nicholas J. Papadopoulos  
; TITLE OF INVENTION: VEGF TRAPS AND THERAPEUTIC USES THEREOF  
; FILE REFERENCE: REG 710D  
; CURRENT APPLICATION NUMBER: US/10/609,775  
; CURRENT FILING DATE: 2003-06-30  
; PRIOR FILING DATE: 10/009,852  
; PRIOR FILING DATE: 2001-12-06  
; PRIOR APPLICATION NUMBER: PCT/US00/14142  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/138,133  
; PRIOR FILING DATE: 1999-06-08  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 458  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-609-775-10

Query Match 100.0%; Score 2437; DB 15; Length 458;  
Best Local Similarity 100.0%; Pred. No. 3.5e-152;  
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MVS YWDTGVLLCALLSCLLLTGSSGSDTGRPFVEMYSEIPIIHMTEGRELVI PCRVTS 60  
Db 1 MVS YWDTGVLLCALLSCLLLTGSSGSDTGRPFVEMYSEIPIIHMTEGRELVI PCRVTS 60  
Qy 61 PNITVTLKKFPLDTLIPDGKRIIWDNRKGFIIISNATYKEIGLLTCEATVNGHLYKTNLYT 120  
Db 61 PNITVTLKKFPLDTLIPDGKRIIWDNRKGFIIISNATYKEIGLLTCEATVNGHLYKTNLYT 120  
Qy 121 HROTNTIIDVVLSPSHGIELSVGEKLVNCTARTELNVGIDFNWVEYPSKQHKKLVNRD 180  
Db 121 HROTNTIIDVVLSPSHGIELSVGEKLVNCTARTELNVGIDFNWVEYPSKQHKKLVNRD 180  
Qy 181 LKQSGSEMMKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKDKHTHTCPPC 240  
Db 181 LKQSGSEMMKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKDKHTHTCPPC 240  
Qy 241 PAPELLGGPSVFLFPKPKDTLMISTRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 300  
Db 241 PAPELLGGPSVFLFPKPKDTLMISTRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 300  
Qy 301 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 360  
Db 301 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 360  
Qy 361 TLPPSRDELTKNQVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSK 420  
Db 361 TLPPSRDELTKNQVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSK 420  
Qy 421 LTVDKSRWQOQGNVFCSCVMHEALHNNHYTQKSLSLSPGK 458  
Db 421 LTVDKSRWQOQGNVFCSCVMHEALHNNHYTQKSLSLSPGK 458

Qy 301 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 360  
Db 301 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 360  
Qy 361 TLPPSRDELTKNQVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSK 420  
Db 361 TLPPSRDELTKNQVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSK 420  
Qy 421 LTVDKSRWQOQGNVFCSCVMHEALHNNHYTQKSLSLSPGK 458  
Db 421 LTVDKSRWQOQGNVFCSCVMHEALHNNHYTQKSLSLSPGK 458

## RESULT 3

US-10-860-958-2  
; Sequence 2, Application US/10860958  
; Publication No. US20040265309A1  
; GENERAL INFORMATION:  
; APPLICANT: Kandel, Jessica  
; APPLICANT: Holash, Jocelyn  
; APPLICANT: Yamashiro, Darrell  
; APPLICANT: Huang, Jianzhong  
; APPLICANT: Yancopoulos, George  
; APPLICANT: Rudge, John  
; TITLE OF INVENTION: Method of Tumor Regression with VEGF  
; FILE REFERENCE: REG 714A  
; CURRENT APPLICATION NUMBER: US/10/860,958  
; CURRENT FILING DATE: 2004-06-04  
; PRIOR APPLICATION NUMBER: 60/476,425  
; PRIOR FILING DATE: 2003-06-06  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 458  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-860-958-2

Query Match 100.0%; Score 2437; DB 16; Length 458;  
Best Local Similarity 100.0%; Pred. No. 3.5e-152;  
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MVS YWDTGVLLCALLSCLLLTGSSGSDTGRPFVEMYSEIPIIHMTEGRELVI PCRVTS 60  
Db 1 MVS YWDTGVLLCALLSCLLLTGSSGSDTGRPFVEMYSEIPIIHMTEGRELVI PCRVTS 60  
Qy 61 PNITVTLKKFPLDTLIPDGKRIIWDNRKGFIIISNATYKEIGLLTCEATVNGHLYKTNLYT 120  
Db 61 PNITVTLKKFPLDTLIPDGKRIIWDNRKGFIIISNATYKEIGLLTCEATVNGHLYKTNLYT 120  
Qy 121 HROTNTIIDVVLSPSHGIELSVGEKLVNCTARTELNVGIDFNWVEYPSKQHKKLVNRD 180  
Db 121 HROTNTIIDVVLSPSHGIELSVGEKLVNCTARTELNVGIDFNWVEYPSKQHKKLVNRD 180  
Qy 181 LKQSGSEMMKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKDKHTHTCPPC 240  
Db 181 LKQSGSEMMKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKDKHTHTCPPC 240  
Qy 241 PAPELLGGPSVFLFPKPKDTLMISTRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 300  
Db 241 PAPELLGGPSVFLFPKPKDTLMISTRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 300  
Qy 301 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 360  
Db 301 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 360  
Qy 361 TLPPSRDELTKNQVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSK 420  
Db 361 TLPPSRDELTKNQVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSK 420  
Qy 421 LTVDKSRWQOQGNVFCSCVMHEALHNNHYTQKSLSLSPGK 458  
Db 421 LTVDKSRWQOQGNVFCSCVMHEALHNNHYTQKSLSLSPGK 458

Db 421 LTVDKSRWQGNVFCVSMHEALHNHYTKLSLSPGK 458

## RESULT 4

US-10-830-902-2

; Sequence 2, Application US/10830902

; Publication No. US2005004027A1

; GENERAL INFORMATION:

; APPLICANT: Stanley Wiegand

; APPLICANT: Jingtai Cao

; APPLICANT: Claus Cursiefen

; TITLE OF INVENTION: Method of Treating Corneal Transplant

; FILE REFERENCE: REG 713B

; CURRENT APPLICATION NUMBER: US/10/830,902

; CURRENT FILING DATE: 2004-04-23

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 458

; TYPE: PRT

; ORGANISM: homo sapiens

US-10-830-902-2

Query Match 100.0%; Score 2437; DB 17; Length 458;

Best Local Similarity 100.0%; Pred. No. 3.5e-152;

Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVS YWDTGVLLCALLSCLLLTGSSSGSDTGRPPVEMYSEIPIIHTMTEGRELVI PCRVTS 60

|||||

Db 1 MVS YWDTGVLLCALLSCLLLTGSSSGSDTGRPPVEMYSEIPIIHTMTEGRELVI PCRVTS 60

|||||

QY 61 PNITVTLKKFPLD TLIPDGKRIIWD SRKGFIISNATYKEIGLLTCEATVNGHLYKTN YLT 120

|||||

Db 61 PNITVTLKKFPLD TLIPDGKRIIWD SRKGFIISNATYKEIGLLTCEATVNGHLYKTN YLT 120

|||||

QY 121 HRQTNTIIDVLSPSHGIELSVGEKLVNCTARTELNVGIDFNWYPSSSHQHKLVNRD 180

|||||

Db 121 HRQTNTIIDVLSPSHGIELSVGEKLVNCTARTELNVGIDFNWYPSSSHQHKLVNRD 180

|||||

QY 181 LKTSQSGEMKKFLLSTLIDGVTSDOGLYTCAASSGLMTKKNSTFVRVHEKDKHTHTCPPC 240

|||||

Db 181 LKTSQSGEMKKFLLSTLIDGVTSDOGLYTCAASSGLMTKKNSTFVRVHEKDKHTHTCPPC 240

|||||

QY 241 PAPELLGGPSVFLFPKPKD TLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKT 300

|||||

Db 241 PAPELLGGPSVFLFPKPKD TLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKT 300

|||||

QY 301 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVY 360

|||||

Db 301 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVY 360

|||||

QY 361 TLPPSRDELTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 420

|||||

Db 361 TLPPSRDELTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 420

|||||

QY 421 LTVDKSRWQGNVFCVSMHEALHNHYTKLSLSPGK 458

|||||

Db 421 LTVDKSRWQGNVFCVSMHEALHNHYTKLSLSPGK 458

|||||

## RESULT 5

US-10-897-802-2

; Sequence 2, Application US/10897802

; Publication No. US20050032699A1

; GENERAL INFORMATION:

; APPLICANT: Jocelyn Holash

; APPLICANT: Robert Jaffe

; APPLICANT: Limin Hu

; APPLICANT: George D. Yancopoulos

; TITLE OF INVENTION: Composition of a VEGF Antagonist and an Anti-Proliferative Agent

; FILE REFERENCE: REG 715B

; CURRENT APPLICATION NUMBER: US/10/897,802

; CURRENT FILING DATE: 2004-07-23

; PRIOR APPLICATION NUMBER: 60/493,971

; PRIOR FILING DATE: 2003-08-08

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 458

; TYPE: PRT

; ORGANISM: homo sapiens

US-10-897-802-2

Query Match 100.0%; Score 2437; DB 17; Length 458;

Best Local Similarity 100.0%; Pred. No. 3.5e-152;

Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVS YWDTGVLLCALLSCLLLTGSSSGSDTGRPPVEMYSEIPIIHTMTEGRELVI PCRVTS 60

|||||

Db 1 MVS YWDTGVLLCALLSCLLLTGSSSGSDTGRPPVEMYSEIPIIHTMTEGRELVI PCRVTS 60

|||||

QY 61 PNITVTLKKFPLD TLIPDGKRIIWD SRKGFIISNATYKEIGLLTCEATVNGHLYKTN YLT 120

|||||

Db 61 PNITVTLKKFPLD TLIPDGKRIIWD SRKGFIISNATYKEIGLLTCEATVNGHLYKTN YLT 120

|||||

QY 121 HRQTNTIIDVLSPSHGIELSVGEKLVNCTARTELNVGIDFNWYPSSSHQHKLVNRD 180

|||||

Db 121 HRQTNTIIDVLSPSHGIELSVGEKLVNCTARTELNVGIDFNWYPSSSHQHKLVNRD 180

|||||

QY 181 LKTSQSGEMKKFLLSTLIDGVTSDOGLYTCAASSGLMTKKNSTFVRVHEKDKHTHTCPPC 240

|||||

Db 181 LKTSQSGEMKKFLLSTLIDGVTSDOGLYTCAASSGLMTKKNSTFVRVHEKDKHTHTCPPC 240

|||||

QY 241 PAPELLGGPSVFLFPKPKD TLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKT 300

|||||

Db 241 PAPELLGGPSVFLFPKPKD TLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKT 300

|||||

QY 301 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVY 360

|||||

Db 301 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVY 360

|||||

QY 361 TLPPSRDELTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 420

|||||

Db 361 TLPPSRDELTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 420

|||||

QY 421 LTVDKSRWQGNVFCVSMHEALHNHYTKLSLSPGK 458

|||||

Db 421 LTVDKSRWQGNVFCVSMHEALHNHYTKLSLSPGK 458

|||||

## RESULT 6

US-10-880-021-10

; Sequence 10, Application US/10880021

; Publication No. US20050043236A1

; GENERAL INFORMATION:

; APPLICANT: Daly, Thomas J.

; APPLICANT: Fandl, James P.

; APPLICANT: Papadopoulos, Nicholas J.

; TITLE OF INVENTION: VEGF Traps and Therapeutic Uses Thereof

; FILE REFERENCE: REG 710D2

; CURRENT APPLICATION NUMBER: US/10/880,021

; CURRENT FILING DATE: 2004-06-29

; PRIOR APPLICATION NUMBER: 10/609,775

; PRIOR FILING DATE: 2003-06-30

; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 10

; LENGTH: 458

; TYPE: PRT

; ORGANISM: homo sapiens

US-10-880-021-10

Query Match 100.0%; Score 2437; DB 17; Length 458;

Best Local Similarity 100.0%; Pred. No. 3.5e-152;

Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MVSYWDTGVLCCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTGRELVI	PCRVTS	60	
Db	1	MVSYWDTGVLCCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTGRELVI	PCRVTS	60	
QY	61	PNITVTLKFPPLDTLIPDGKRIIWD	SRKGFIIISNATYKEIGLLTCBATVNGHLYKTN	YLT 120	
Db	61	PNITVTLKFPPLDTLIPDGKRIIWD	SRKGFIIISNATYKEIGLLTCBATVNGHLYKTN	YLT 120	
QY	121	HRQTNTIIDVLSPSHGIELSVGEKLVNCTART	ELNVGIDFNWYPS	SSKHQHKLVNRD 180	
Db	121	HRQTNTIIDVLSPSHGIELSVGEKLVNCTART	ELNVGIDFNWYPS	SSKHQHKLVNRD 180	
QY	181	LKTQSGSEMKKFLSTLTIDGVT	RSDOGLYTCASSGLMTKKNSTFVRV	HEKDKTHTCPPC 240	
Db	181	LKTQSGSEMKKFLSTLTIDGVT	RSDOGLYTCASSGLMTKKNSTFVRV	HEKDKTHTCPPC 240	
QY	241	PAPELLGGPSVFLFP	PKPDKTLMISRTPEVTCVVVDVSHEDP	VKFNWYVDGVEVHN	AKT 300
Db	241	PAPELLGGPSVFLFP	PKPDKTLMISRTPEVTCVVVDVSHEDP	VKFNWYVDGVEVHN	AKT 300
QY	301	KPREEQNSTYRVSV	VLTVLHQDWLNGKEYCKVSNKALPAPIE	KTISAKAGQPREPQVY 360	
Db	301	KPREEQNSTYRVSV	VLTVLHQDWLNGKEYCKVSNKALPAPIE	KTISAKAGQPREPQVY 360	
QY	361	TLPPSRDELTKNQVSLTCLVKGP	YPSDIAVEMESNGQPENNYKTTPPVLDSDG	SFFLYSK 420	
Db	361	TLPPSRDELTKNQVSLTCLVKGP	YPSDIAVEMESNGQPENNYKTTPPVLDSDG	SFFLYSK 420	
QY	421	LTVDKSRWQQGNV	FSCSVNHEALHNHYTQKSLSLSPGK	458	
Db	421	LTVDKSRWQQGNV	FSCSVNHEALHNHYTQKSLSLSPGK	458	
RESULT 7					
US-10-909-011-4					
; Sequence 4, Application US/10909011					
; Publication No. US20050112061A1					
; GENERAL INFORMATION:					
; APPLICANT: Jocelyn Holash					
; APPLICANT: George Yancopoulos					
; APPLICANT: Phyllis R. Wachsberger					
; APPLICANT: Adam P. Dicker					
; APPLICANT: Randy Burd					
; TITLE OF INVENTION: Use of a VEGF Antagonist in Combination with Radiation Therapy					
; FILE REFERENCE: REG 716A					
; CURRENT APPLICATION NUMBER: US/10/909,011					
; CURRENT FILING DATE: 2004-07-30					
; PRIOR APPLICATION NUMBER: 60/492,864					
; PRIOR FILING DATE: 2003-08-06					
; NUMBER OF SEQ ID NOS: 4					
; SOFTWARE: FastSeq for Windows Version 4.0					
; SEQ ID NO 4					
; LENGTH: 458					
; TYPE: PRT					
; ORGANISM: homo sapiens					
US-10-909-011-4					
Query Match					
Best Local Similarity 100.0%; Score 2437; DB 17; Length 458;					
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1	MVSYWDTGVLCCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTGRELVI	PCRVTS	60	
Db	1	MVSYWDTGVLCCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTGRELVI	PCRVTS	60	
QY	61	PNITVTLKFPPLDTLIPDGKRIIWD	SRKGFIIISNATYKEIGLLTCBATVNGHLYKTN	YLT 120	
Db	61	PNITVTLKFPPLDTLIPDGKRIIWD	SRKGFIIISNATYKEIGLLTCBATVNGHLYKTN	YLT 120	
QY	121	HRQTNTIIDVLSPSHGIELSVGEKLVNCTART	ELNVGIDFNWYPS	SSKHQHKLVNRD 180	
Db	121	HRQTNTIIDVLSPSHGIELSVGEKLVNCTART	ELNVGIDFNWYPS	SSKHQHKLVNRD 180	

QY	181	LKTQSGSEMKKFLSTLTIDGVT	RSDOGLYTCASSGLMTKKNSTFVRV	HEKDKTHTCPPC	240
Db	181	LKTQSGSEMKKFLSTLTIDGVT	RSDOGLYTCASSGLMTKKNSTFVRV	HEKDKTHTCPPC	240
QY	241	PAPELLGGPSVFLFP	PKPDKTLMISRTPEVTCVVVDVSHEDP	VKFNWYVDGVEVHN	AKT 300
Db	241	PAPELLGGPSVFLFP	PKPDKTLMISRTPEVTCVVVDVSHEDP	VKFNWYVDGVEVHN	AKT 300
QY	301	KPREEQNSTYRVSV	VLTVLHQDWLNGKEYCKVSNKALPAPIE	KTISAKAGQPREPQVY	360
Db	301	KPREEQNSTYRVSV	VLTVLHQDWLNGKEYCKVSNKALPAPIE	KTISAKAGQPREPQVY	360
QY	361	TLPPSRDELTKNQVSLTCLVKGF	YPSDIAVEMESNGQPENNYKTTPVLDSDG	SFFLYSK	420
Db	361	TLPPSRDELTKNQVSLTCLVKGF	YPSDIAVEMESNGQPENNYKTTPVLDSDG	SFFLYSK	420
QY	421	LTVDKSRWQQGNV	FSCSVNHEALHNHYTQKSLSLSPGK	458	
Db	421	LTVDKSRWQQGNV	FSCSVNHEALHNHYTQKSLSLSPGK	458	
RESULT 8					
US-10-988-243-16					
; Sequence 16, Application US/10988243					
; Publication No. US20050175610A1					
; GENERAL INFORMATION:					
; APPLICANT: Wiegand, Stanley					
; APPLICANT: Yancopoulos, George					
; TITLE OF INVENTION: Modified Chimeric Polypeptides with Improved Pharmacokinetic Properties					
; TITLE OF INVENTION: and Methods of Making and Using Thereof					
; FILE REFERENCE: REG 710F					
; CURRENT APPLICATION NUMBER: US/10/988,243					
; PRIOR FILING DATE: 2004-11-12					
; PRIOR APPLICATION NUMBER: 10/009,852					
; PRIOR FILING DATE: 2001-12-06					
; PRIOR APPLICATION NUMBER: PCT/US00/14142					
; PRIOR FILING DATE: 2000-05-23					
; PRIOR APPLICATION NUMBER: 60/138,133					
; PRIOR FILING DATE: 1999-06-08					
; NUMBER OF SEQ ID NOS: 35					
; SOFTWARE: FastSeq for Windows Version 4.0					
; SEQ ID NO 16					
; LENGTH: 458					
; TYPE: PRT					
; ORGANISM: Homo sapiens					
US-10-988-243-16					
Query Match					
Best Local Similarity 100.0%; Score 2437; DB 18; Length 458;					
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1	MVSYWDTGVLCCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTGRELVI	PCRVTS	60	
Db	1	MVSYWDTGVLCCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIIHMTGRELVI	PCRVTS	60	
QY	61	PNITVTLKFPPLDTLIPDGKRIIWD	SRKGFIIISNATYKEIGLLTCBATVNGHLYKTN	YLT	120
Db	61	PNITVTLKFPPLDTLIPDGKRIIWD	SRKGFIIISNATYKEIGLLTCBATVNGHLYKTN	YLT	120
QY	121	HRQTNTIIDVLSPSHGIELSVGEKLVNCTART	ELNVGIDFNWYPS	SSKHQHKLVNRD	180
Db	121	HRQTNTIIDVLSPSHGIELSVGEKLVNCTART	ELNVGIDFNWYPS	SSKHQHKLVNRD	180
QY	181	LKTQSGSEMKKFLSTLTIDGVT	RSDOGLYTCASSGLMTKKNSTFVRV	HEKDKTHTCPPC	240
Db	181	LKTQSGSEMKKFLSTLTIDGVT	RSDOGLYTCASSGLMTKKNSTFVRV	HEKDKTHTCPPC	240
QY	241	PAPELLGGPSVFLFP	PKPDKTLMISRTPEVTCVVVDVSHEDP	VKFNWYVDGVEVHN	AKT 300
Db	241	PAPELLGGPSVFLFP	PKPDKTLMISRTPEVTCVVVDVSHEDP	VKFNWYVDGVEVHN	AKT 300



Qy 301 KPREEQNSTYRVVSVLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSK 360  
Db 301 KPREEQNSTYRVVSVLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSK 360  
Qy 361 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSK 420  
Db 361 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSK 420  
Qy 421 LTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK 458  
Db 421 LTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK 458

RESULT 9  
US-10-998-881-4  
; Sequence 4, Application US/10998881  
; Publication No. US20050196340A1  
; GENERAL INFORMATION:  
; APPLICANT: Jocelyn Holash  
; APPLICANT: George Yancopoulos  
; APPLICANT: Phyllis R. Wachsberger  
; APPLICANT: Adam P. Dicker  
; APPLICANT: Randy Burd  
; TITLE OF INVENTION: Use of a VEGF Antagonist in Combination with Radiation Therapy  
; FILE REFERENCE: 716B  
; CURRENT APPLICATION NUMBER: US/10/998,881  
; CURRENT FILING DATE: 2004-11-29  
; PRIOR APPLICATION NUMBER: 10/909,011  
; PRIOR FILING DATE: 2004-07-30  
; PRIOR APPLICATION NUMBER: 60/492,864  
; PRIOR FILING DATE: 2003-08-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: Fast-Seq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 458  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-998-881-4

Query Match 100.0%; Score 2437; DB 18; Length 458;  
Best Local Similarity 100.0%; Pred. No. 3.5e-152;  
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVS YMDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIHHMTEGRELVI PCRVTS 60  
Db 1 MVS YMDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIHHMTEGRELVI PCRVTS 60  
Qy 61 PNITVTLKKPPLDPLIPDGKRIIWDNRKGFIIISNATYKEIGLLTCEATVNGHLYKTNLT 120  
Db 61 PNITVTLKKPPLDPLIPDGKRIIWDNRKGFIIISNATYKEIGLLTCEATVNGHLYKTNLT 120  
Qy 121 HRQTNTIIDVLSPSHGIELSVGEKLVNCTARTELNVGIDFNWEPSSKHQHKLVNRD 180  
Db 121 HRQTNTIIDVLSPSHGIELSVGEKLVNCTARTELNVGIDFNWEPSSKHQHKLVNRD 180  
Qy 181 LKTSQSEMKKFSLTITIDGVTSDOGLYTCAASSGLMTKKNSTFVRVHEKDKHTHTCPPC 240  
Db 181 LKTSQSEMKKFSLTITIDGVTSDOGLYTCAASSGLMTKKNSTFVRVHEKDKHTHTCPPC 240  
Qy 241 PAPELLGGPSVFLPPKPKDPLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT 300  
Db 241 PAPELLGGPSVFLPPKPKDPLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT 300  
Qy 301 KPREEQNSTYRVVSVLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSK 420  
Db 301 KPREEQNSTYRVVSVLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSK 420  
Qy 421 LTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK 458  
Db 421 LTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK 458

Db 421 LTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK 458

RESULT 10  
US-11-016-097-16  
; Sequence 16, Application US/11016097  
; Publication No. US20050163798A1  
; GENERAL INFORMATION:  
; APPLICANT: Nicholas J. Papadopoulos et al.  
; TITLE OF INVENTION: MODIFIED CHIMERIC POLYPEPTIDES WITH IMPROVED  
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES AND METHODS OF MAKING  
; TITLE OF INVENTION: AND USING THEREOF  
; FILE REFERENCE: REG 710-A-US  
; CURRENT APPLICATION NUMBER: US/11/016,097  
; CURRENT FILING DATE: 2004-12-17  
; PRIOR APPLICATION NUMBER: US/10/009,852  
; PRIOR FILING DATE: 2001-12-06  
; PRIOR APPLICATION NUMBER: PCT/US00/14142  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/138,133  
; PRIOR FILING DATE: 1999-06-08  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: Fast-Seq for Windows Version 3.0  
; SEQ ID NO 16  
; LENGTH: 458  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-016-097-16

Query Match 100.0%; Score 2437; DB 20; Length 458;  
Best Local Similarity 100.0%; Pred. No. 3.5e-152;  
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVS YMDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIHHMTEGRELVI PCRVTS 60  
Db 1 MVS YMDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPEIHHMTEGRELVI PCRVTS 60  
Qy 61 PNITVTLKKPPLDPLIPDGKRIIWDNRKGFIIISNATYKEIGLLTCEATVNGHLYKTNLT 120  
Db 61 PNITVTLKKPPLDPLIPDGKRIIWDNRKGFIIISNATYKEIGLLTCEATVNGHLYKTNLT 120  
Qy 121 HRQTNTIIDVLSPSHGIELSVGEKLVNCTARTELNVGIDFNWEPSSKHQHKLVNRD 180  
Db 121 HRQTNTIIDVLSPSHGIELSVGEKLVNCTARTELNVGIDFNWEPSSKHQHKLVNRD 180  
Qy 181 LKTSQSEMKKFSLTITIDGVTSDOGLYTCAASSGLMTKKNSTFVRVHEKDKHTHTCPPC 240  
Db 181 LKTSQSEMKKFSLTITIDGVTSDOGLYTCAASSGLMTKKNSTFVRVHEKDKHTHTCPPC 240  
Qy 241 PAPELLGGPSVFLPPKPKDPLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT 300  
Db 241 PAPELLGGPSVFLPPKPKDPLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKT 300  
Qy 301 KPREEQNSTYRVVSVLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSK 420  
Db 301 KPREEQNSTYRVVSVLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSK 420  
Qy 421 LTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK 458  
Db 421 LTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK 458

RESULT 11  
US-11-039-144-2  
; Sequence 2, Application US/11039144  
; Publication No. US20050197291A1  
; GENERAL INFORMATION:  
; APPLICANT: Stanley Wiegand  
; APPLICANT: Jingtai Cao

```
; APPLICANT: Claus Cursiefen
; TITLE OF INVENTION: Method of Treating Corneal Transplant
; FILE REFERENCE: 713C
; CURRENT APPLICATION NUMBER: US/11/039,144
; PRIOR FILING DATE: 2005-01-19
; PRIOR APPLICATION NUMBER: 10/830,902
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: 60/473,734
; PRIOR FILING DATE: 2003-05-28
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 458
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-039-144-2

Query Match      100.0%; Score 2437; DB 20; Length 458;
Best Local Similarity 100.0%; Pred. No. 3.5e-152;
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVS YWDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPIIHMTEGRELVIPCRVTS 60
DB 1 MVS YWDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPIIHMTEGRELVIPCRVTS 60

QY 61 PNI TVTLKKFPPLDTLIPDGKRIIWSRKGFIIISNATYKEIGLLTCEATVNGHLYKTNLYT 120
DB 61 PNI TVTLKKFPPLDTLIPDGKRIIWSRKGFIIISNATYKEIGLLTCEATVNGHLYKTNLYT 120

QY 121 HRQTNTIIDVLSPSHGIELSVGEKLVNCTARTELNVGIDFNWYEPSSKHQHKLVNRD 180
DB 121 HRQTNTIIDVLSPSHGIELSVGEKLVNCTARTELNVGIDFNWYEPSSKHQHKLVNRD 180

QY 181 LKTQSGSEMKKFLSTLTIDGVTNRSDQGLYTCAASSGLMTKKNSTFVRVHEK---DKTHTC 237
DB 181 LKTQSGSEMKKFLSTLTIDGVTNRSDQGLYTCAASSGLMTKKNSTFVRVHEK---DKTHTC 237

QY 238 PPCAPELGGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 297
DB 238 PPCAPELGGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 297

QY 298 AKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISAKAGQPREP 357
DB 298 AKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISAKAGQPREP 357

QY 358 QYTVLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPL 417
DB 358 QYTVLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFPL 417

QY 418 YSKLTVDSRWQGNVFCSCVMHEALHNHYTOKSLSPGK 458
DB 418 YSKLTVDSRWQGNVFCSCVMHEALHNHYTOKSLSPGK 458

RESULT 13
US-10-609-775-8
; Sequence 8, Application US/10609775
; Publication No. US20040014667A1
; GENERAL INFORMATION:
; APPLICANT: Thomas J. Daly
; APPLICANT: James P. Fandl
; APPLICANT: Nicholas J. Papadopoulos
; TITLE OF INVENTION: VEGF TRAPS AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: REG 710D
; CURRENT APPLICATION NUMBER: US/10/609,775
; CURRENT FILING DATE: 2003-06-30
; PRIOR APPLICATION NUMBER: 10/009,852
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/14142
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/138,133
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 458
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-609-775-8

Query Match      98.4%; Score 2399; DB 15; Length 458;
Best Local Similarity 98.7%; Pred. No. 1.1e-149;
Matches 455; Conservative 0; Mismatches 0; Indels 6; Gaps 2;

QY 1 MVS YWDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPIIHMTEGRELVIPCRVTS 60
DB 1 MVS YWDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPIIHMTEGRELVIPCRVTS 57

; APPLICANT: Claus Cursiefen
; TITLE OF INVENTION: Method of Treating Corneal Transplant
; FILE REFERENCE: 713C
; CURRENT APPLICATION NUMBER: US/11/039,144
; PRIOR FILING DATE: 2005-01-19
; PRIOR APPLICATION NUMBER: 10/830,902
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: 60/473,734
; PRIOR FILING DATE: 2003-05-28
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 458
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-039-144-2

Query Match      100.0%; Score 2437; DB 20; Length 458;
Best Local Similarity 100.0%; Pred. No. 3.5e-152;
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVS YWDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPIIHMTEGRELVIPCRVTS 60
DB 1 MVS YWDTGVLLCALLSCLLLTGSSSGSDTGRPFVEMYSEIPIIHMTEGRELVIPCRVTS 60

QY 61 PNI TVTLKKFPPLDTLIPDGKRIIWSRKGFIIISNATYKEIGLLTCEATVNGHLYKTNLYT 120
DB 61 PNI TVTLKKFPPLDTLIPDGKRIIWSRKGFIIISNATYKEIGLLTCEATVNGHLYKTNLYT 120

QY 121 HRQTNTIIDVLSPSHGIELSVGEKLVNCTARTELNVGIDFNWYEPSSKHQHKLVNRD 180
DB 121 HRQTNTIIDVLSPSHGIELSVGEKLVNCTARTELNVGIDFNWYEPSSKHQHKLVNRD 180

QY 181 LKTQSGSEMKKFLSTLTIDGVTNRSDQGLYTCAASSGLMTKKNSTFVRVHEKDKTHTC 240
DB 181 LKTQSGSEMKKFLSTLTIDGVTNRSDQGLYTCAASSGLMTKKNSTFVRVHEKDKTHTC 240

QY 241 PAPELLGGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 300
DB 241 PAPELLGGPSVFLFPKPKDTLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 300

QY 301 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISAKAGQPREPQVY 360
DB 301 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISAKAGQPREPQVY 360

QY 361 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYXK 420
DB 361 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYXK 420

QY 421 LTVDSRWQGNVFCSCVMHEALHNHYTOKSLSPGK 458
DB 421 LTVDSRWQGNVFCSCVMHEALHNHYTOKSLSPGK 458

RESULT 12
US-09-773-877A-22
; Sequence 22, Application US/09773877A
; Publication No. US2003001797A1
; GENERAL INFORMATION:
; APPLICANT: Xia, Yu-Ping et al.
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
; FILE REFERENCE: REG 710b
; CURRENT APPLICATION NUMBER: US/09/773,877A
; CURRENT FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: F1t1D2.F1k1D3.FcdeltaC1(a) Receptor
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QY 61 PNITVTLLKFPPLDTLIPDGKRIIWDNRKGFIIISNATYKEIGLLTCEATVNGHLYKTNLYT 120
Db 58 PNITVTLLKFPPLDTLIPDGKRIIWDNRKGFIIISNATYKEIGLLTCEATVNGHLYKTNLYT 117
QY 121 HROTNTIIDVVLSPSHGIELSVGEKLVNCTARTELNVGIDFNWEPSSKHQHKLVNRD 180
Db 118 HROTNTIIDVVLSPSHGIELSVGEKLVNCTARTELNVGIDFNWEPSSKHQHKLVNRD 177
QY 181 LKTQSGEMKKFLLSTLTIDGVTSDOGLYTCAASSGLMTKKNSTFVRVHEK---DKTHTC 237
Db 178 LKTQSGEMKKFLLSTLTIDGVTSDOGLYTCAASSGLMTKKNSTFVRVHEKGPDKTHTC 237
QY 238 PPCPAPELLGGPSVFLPPPKPDTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 297
Db 238 PPCPAPELLGGPSVFLPPPKPDTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 297
QY 298 AKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREP 357
Db 298 AKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREP 357
QY 358 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 417
Db 358 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 417
QY 418 YSKLTVDKSRWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 458
Db 418 YSKLTVDKSRWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 458

RESULT 14
US-10-880-021-8
; Sequence 8, Application US/10880021
; Publication No. US20050043236A1
; GENERAL INFORMATION:
; APPLICANT: Daly, Thomas J.
; APPLICANT: Pandl, James P.
; APPLICANT: Papadopoulos, Nicholas J.
; TITLE OF INVENTION: VEGF Traps and Therapeutic Uses Thereof
; FILE REFERENCE: RGE 710D2
; CURRENT APPLICATION NUMBER: US/10/880,021
; CURRENT FILING DATE: 2004-06-29
; PRIOR APPLICATION NUMBER: 10/609,775
; PRIOR FILING DATE: 2003-06-30
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 458
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-880-021-8

Query Match 98.4%; Score 2399; DB 17; Length 458;
Best Local Similarity 98.7%; Pred. No. 1.1e-149;
Matches 455; Conservative 0; Mismatches 0; Indels 6; Gaps 2;

QY 1 MVS YMDTGVLVLCALLSCLLLTGSSGSDTGRPFVEMYSEIPIIHMTEGRELVI PCRVTS 60
Db 1 MVS YMDTGVLVLCALLSCLLLTGSSG--GRPFVEMYSEIPIIHMTEGRELVI PCRVTS 57
QY 61 PNITVTLLKFPPLDTLIPDGKRIIWDNRKGFIIISNATYKEIGLLTCEATVNGHLYKTNLYT 120
Db 58 PNITVTLLKFPPLDTLIPDGKRIIWDNRKGFIIISNATYKEIGLLTCEATVNGHLYKTNLYT 117
QY 121 HROTNTIIDVVLSPSHGIELSVGEKLVNCTARTELNVGIDFNWEPSSKHQHKLVNRD 180
Db 118 HROTNTIIDVVLSPSHGIELSVGEKLVNCTARTELNVGIDFNWEPSSKHQHKLVNRD 177
QY 181 LKTQSGEMKKFLLSTLTIDGVTSDOGLYTCAASSGLMTKKNSTFVRVHEK---DKTHTC 237
Db 178 LKTQSGEMKKFLLSTLTIDGVTSDOGLYTCAASSGLMTKKNSTFVRVHEKGPDKTHTC 237
QY 238 PPCPAPELLGGPSVFLPPPKPDTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 297
Db 238 PPCPAPELLGGPSVFLPPPKPDTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 297
QY 298 AKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREP 357
Db 298 AKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREP 357
QY 358 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 417
Db 358 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 417
QY 418 YSKLTVDKSRWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 458
Db 418 YSKLTVDKSRWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 458
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Db 238 PPCPAPELLGGPSVFLPPPKPDTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 297
QY 298 AKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREP 357
Db 298 AKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREP 357
QY 358 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 417
Db 358 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 417
QY 418 YSKLTVDKSRWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 458
Db 418 YSKLTVDKSRWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 458

RESULT 15
US-10-909-011-2
; Sequence 2, Application US/10909011
; Publication No. US20050112061A1
; GENERAL INFORMATION:
; APPLICANT: Jocelyn Holash
; APPLICANT: George Yancopoulos
; APPLICANT: Phyllis R. Wachsberger
; APPLICANT: Adam P. Dicker
; APPLICANT: Randy Burd
; TITLE OF INVENTION: Use of a VEGF Antagonist in Combination with Radiation Therapy
; FILE REFERENCE: REG 716A
; CURRENT APPLICATION NUMBER: US/10/909,011
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/492,864
; PRIOR FILING DATE: 2003-08-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 458
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-909-011-2

Query Match 98.4%; Score 2399; DB 17; Length 458;
Best Local Similarity 98.7%; Pred. No. 1.1e-149;
Matches 455; Conservative 0; Mismatches 0; Indels 6; Gaps 2;

QY 1 MVS YMDTGVLVLCALLSCLLLTGSSGSDTGRPFVEMYSEIPIIHMTEGRELVI PCRVTS 60
Db 1 MVS YMDTGVLVLCALLSCLLLTGSSG--GRPFVEMYSEIPIIHMTEGRELVI PCRVTS 57
QY 61 PNITVTLLKFPPLDTLIPDGKRIIWDNRKGFIIISNATYKEIGLLTCEATVNGHLYKTNLYT 120
Db 58 PNITVTLLKFPPLDTLIPDGKRIIWDNRKGFIIISNATYKEIGLLTCEATVNGHLYKTNLYT 117
QY 121 HROTNTIIDVVLSPSHGIELSVGEKLVNCTARTELNVGIDFNWEPSSKHQHKLVNRD 180
Db 118 HROTNTIIDVVLSPSHGIELSVGEKLVNCTARTELNVGIDFNWEPSSKHQHKLVNRD 177
QY 181 LKTQSGEMKKFLLSTLTIDGVTSDOGLYTCAASSGLMTKKNSTFVRVHEK---DKTHTC 237
Db 178 LKTQSGEMKKFLLSTLTIDGVTSDOGLYTCAASSGLMTKKNSTFVRVHEKGPDKTHTC 237
QY 238 PPCPAPELLGGPSVFLPPPKPDTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 297
Db 238 PPCPAPELLGGPSVFLPPPKPDTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 297
QY 298 AKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREP 357
Db 298 AKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREP 357
QY 358 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 417
Db 358 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 417
QY 418 YSKLTVDKSRWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 458
Db 418 YSKLTVDKSRWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 458
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Db 418 YSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPCK 458

Search completed: September 23, 2005, 17:21:05  
Job time : 125 secs

## Protein Sequence Searches - February 2005

10/811,170

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

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